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AB059554 Mus muscu BX322642 Mus muscu Continuation (3 of Continuation (3 of AL772303 Mouse DNA ACL20773 Rattus no AC899423 Rattus no AJ699423 Rattus no AJ699423 Rattus no AJ699424 Rattus no AJ697663 Pan trogl AJ694413 Bos teuru CQ736679 Sequence AL158164 Human DNA AJ699424 Gallus ga CR352448 Gallus ga AC143457 Macaca mu BV211170 SIATBF 5 AJ704564 Gallus ga
                                                                     May 31, 2006, 10:18:03 ; Search time 17609 Seconds (without alignments) 11497.390 Million cell updates/sec
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                                                                                                                                                1 cggagcgagtcgagtcgcc......gctattagcaaaaaaaa 3166
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                                                                                                                                                                                                                                     12732272
GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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| /translation="MRSGGTLFALIGSLMLLLLLRMLWCPADAPARSRLLMEGSREDT SGTSAALKTLWSPTTPVPRTRNSTYLDEKTTQITEKCKDLOYSLNSLSNKTRYSEDD SGTSAALKTLWSPTTPVPRTRLASCCDALODFVVSQNNTPVGTNNSYEVESKK HIPIRENIFWPFPVSOPFVDYPYNOCAVCNGGTLNKSLCGSEIDKSDFYPRCNLPPI TGSASKDVGSKTNLVTVNP9IITLKKQNLKEKKAOFLEDISTYGDAFLLLPPI TGSASKDVGSKTNLVTVNP9IITLKKQNLKEKKAOFLEDISTYGDAFLLLPAFSYRAN TGISFKVYQTLKESKWRQKVLFFHRYLHHALFWRTKGVTAYRLSTGLMIASVAVEL CENYKLYGFWPFSKTIEDTPLSHHYYDNMLPKHGFHQMPKEYSQMLQLHWRGILKLQF SKCETA" | Query Match 100.0%; Score 3166; DB 6; Length 3166; Best Local Similarity 100.0%; Pred; No. 0; No. 0; Matches 3166; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 CGGAGGGGGAGTGCGCCCGGGCTGCGCTTGCCCCGGCAGGGGGGGG | Db 1 cásaccáscasírásasírásasárásasírásasárástrasásáratrásásárásasá 60 Qy 61 accacagasatasatasatasatasástrasásasásasásasásasásasásasásasásasásasá | 121 GCTGCTGCTCTGCGTATGCTCTGGTGCCCAGCGGCGGCCTGCCCGCTCCAGGCT | 181 GITGAIGGAGGAGGAGGAGGACACCAGIGGIACCICAGCIGCACTGAGGACACTCIG 241 GAGCCCGACAACCCGGIACCACGCACACAGGAACAGACAIAICTGGAIGAGAGACAAC 241 GAGCCCGACAACCCCGGIACCACGCACCAGGAACAGCACAIAICTGGAIGAGAAGACAAC | Oy 301 CCAAATAACAGAGAAATGCAAAGATCTTGCAATATCTTAACAAAAC 360 Db 301 CCAAATAACAGAGAAATGCAAATATAGCTTGAACTCTTTATCTAACAAAAC 360 Oy 361 GAGACGGTACTCTGAGAATGACTACCTCCAAACATACATA | OY 421 GAACCGGCAAGCAGAATATGACAATTTTAGAGCAAAACTGGCTTCCTGTTGCGATGC 480 Db 421 GAACCGGCAAGCAAGAAATATGACAATTTTAGAGCAAAACTGGCTTCCTGTTGCGATGC 480 OY 481 CATTCAAGACTTCGTGGTTTCCCAGAACAACTCCGTGGGGACTAACATGAGCTACGATGC 540 Db 481 CATTCAAGACTTCGTGGTTTCCCAGAACAACACTCCAGTGGGGACTAACATGAGCTACAG 540 OY 541 GGTGGAAAGCAAGAACAACCCCATTCGAGAGAACAATTCCACATGTTTTCCACATGTTTTCCACATACAT | 00 00 00 00 00 00 00 0 | 721 CCCCCAATCACAGGAGCGTTAGTAAGATGTTGGAAGCAAAACAAATCTTGTGACTGT 721 CCCCCCAATCACAGGAGCGCTAGTAAAGATGTTGGAAGCAAAACAAATCTTGTGACTGT 721 CCCCCCAATCACAGGAGCGCTAGTAAAGATGTTGGAAGCAAAACAAATCTTGTGACTGT 781 CAATCCCAGCATTATAACCCTGAAGTACCAGAATTTGAAGGAAAAAAAA |

| TTTTAAAGTCTACCAAACACTCAAAGAGTCAAAAATGAGGCAAAA 9 | TIIIII [[| ccaggaactractractritttaaaactaaagg | AGGCTTGATGATTGCAAGTGTCGCTGTGGAACTGTG | CTGGCCTTTCTCTAAGACTATCGAAGACACCCCACT | NTAACATGETTACCTAAGCATGGTTTCCACCAGATGCCTAAAGA 1200 | (tatgagagaatcctcaaactgcaattcagcaaatg | agagaataatttcagaaggtgaagtgaatgtgtg | agaagggacagagaaggatgaattacaaaggcgct | ACCGCCCCACTCACTTTGCAGCCTCCACGAGTCA | TCTCTGAGAATAGAGCCAAAACATCAGACTTGGAT | ATCATCATAGATTTGATTTGACCAGGGTCTCTCA | ratagccattcccaccttatcacactggaatgaa | TTTCTGAAGAGAATGTCTGAATCATGCGCCGAGTTT | AATAAATCCTTCCCATTCTCCCTCCTAGTAGAGTACA | aggaagaaagtctttttacttagcaatgtgcctg | ATTAAGCTGGGGTTTTGGTTGGATTTGGGGCC | CTATATITECTTACCTTTATCAGTTTGTATTCGAGCTTCC 1920 | CTCCCACTGACAGGATCAACTCAATGACATAAAGTA 1 |
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| CAACACAGGCATCTC | CAACACAGGCATCTCT | GGTTCTCTTCCAT | GGTGACTGCATACCGCT | TGAAAACGTGAAGCTCT. TGAAAACGTGAAGCTCT. | CAGTCACCACTACTATGA | ATACAGCCAAATGCTCCA | TGAAACGGCTTAACGTTT TGAAACGGCTTAACGTTT | CAGCATCTCCAAAAAGCC | crcccacrrgrcragacc | CTCATTCTCACCTTCAAC | aagtaaaatgagataatt | GAATGCTTCCTTGTTCCTP | actgtgcaattgtgccaaa | TTACACACGCTCTTCCTT | GAAACAAATACCCTTGATC | CTTCTGATTCAGTTCGCTT | GTTTCTTCACTTCTTTTGT | TGCTTTGGGATTCTGCAAT |
| 901 CAACACAGGCATCTC | - 6 | 961 GGITCICITCITCCAICCAGGGGGGGGGGGGGGGGGGGGG | 1021 GGTGACTGCATACCGC | 1081 TGAAACGTGAAGCTCTACGGATT | 41 | 1201 ATACAGCCAAATGCTCCAGCTCC | 1261 TGAAACGCTTAACGTTT | 21 | 1381 CTCCCACTTGTCTAGACCAAAGCT | 41 | 0 0 | 61 | 1621 ACTGTGCAATTGTGCCAAAGAC | 1681 TTACACACAGCTCTTCCTT | 1741 GAAACAAAATACCCTTGATGAT | 1801 CTTCTGATTCAGTTCGCTT | 1861 GTTTCTTCACTTCTTTTGT 1861 GTTTCTTCACTTCTTTTGT | 1921 TGCTTTGGGATTCTGCAATTCT |

| CTCTITTATGC GCTGCTAATGAACCTAATTAGCTTTAAATTATCTCCT 3120 TCACGTTTCAA CATGCTATTAGCAAAAAAAA 3166 | TUS BX322642 Acces 000 000 000 000 000 | chromosome ; clone RP24-36309, WORKING DRAFT SEQUENCE, vieces. G1:86476683 G2:8647683 G1:8647683 Chouse mouse tazoa; Chorqta; Craniata; Vertebrata; Euteleostomi; hexia: Euromotoglires: Glires: Rodentia: | nridae; Murinae; Mus ellcome Trust Sanger UK. B-mail enquirles | | stics sion 4.5 00% of reads ses at least Q40 ses at least Q20 contigs rror; agarose-fp | age: 0.40% to 020 bases; sum-or-contigs quality is in Q20 bases; agarose-fp is a 'working draft' sequence. It currently b contigs. The true order of the pieces and their brder in this sequence record is and their brder in this sequence record is apps between the contigs are represented as wit he exact sizes of the gaps are unknown. will be upquted with the finished sequence it is available and the accession number will | ad. 163997; cont.g of 163997 bp in length 164087; gap of 100 bp 166408; cont.g of 2311 bp in length 166509; gap of 101 bp 170150; gap of 101 bp 170150; gap of 100 bp 214118; cont.g of 43868 bp in length 214118; cont.g of 18664 bp in length 232782; cont.g of 18654 bp in length 232782; cont.g of 18579 bp in length 258463; cont.g of 25579 bp in length |
|--|--|--|---|--|--|--|--|
| 0 Db 3061 ATGAATAGAGGCTCTTTTATGC 0 Oy 3121 AGCAACATTGGTCACGTTTCAA 0 Db 3121 AGCAACATTGGTCACGTTTCAA | RESULT 2 BX322642 0/C WPCOMMENT Sequence split into 5 Fragment Name BX322642 0 BX322642 1 BX322642 2 BX322642 3 BX322642 3 BX322642 3 BX322642 3 | DEFINITION WAS TRECULED BEFINITION WAS TRECULED BY STATE OF STA | REFERENCE 1 (bases 1 to AUTHORS 1109d, D. TITLE Direct Submiss JOURNAL Submitted (02-cambridgesbire Clone requests | COMMENT On Feb 4, 2006 Center: Wellcr Center code: 6 Web site: bitg Contact: vegad | | | |
| 1981 GTTCAAACATCCATTGCTTCTCACATGTTTTATCCATAAAGTTACTCATCTGATTTTATT 2040 1981 GTTCAAACATCCATTGCTTCTCACATGTTTTATCCATAAAGTTACTCATCTGATTTTATT 2040 2041 TAAAATAGTGAACATCTACTTGATATCAGACCCGAGGACCATCCCATTGGAGAATATG 2100 2041 TAAAATAGTGAACATCTACTTGATATCAGACCAGAGGACCATCCCATTGGAGAATATG 2100 2041 TAAAATAGTGAACATCTACTTGATATCAGACCAGGGACCATCCCCATTGGAGAATATG 2100 | AGGITATIGICACTGGCAGAAAAGCGGGTGTGCCATTAATTGATAAGATACCACAAGC | 2281 AACTAGTAAATGAACCAATTCTTAGGCACATTAAGTGGATTCTGAGTAAAAGGAA 2340 2281 AACTAGTAAATGAACCAATTCTTAGGCACATTAAGTGGATTCTGAGTAAAAGAAAG | 2401 TGTGAGGCTACAAAACCTCTGCGTAGGAGAGAGAGTACAGTGCATGAGTGTGCCGGCT 2460 2401 TGTGAGGCTAAAACCTCTGCGTAGAGAGAGAGAGAGTGTGTGT | 2521 ACCTAACTCATCACGGGGGAGATGAATGCTTTCATGAGAATTACACTCATAAGCT 2580 [| 2641 CTAATGTCCCACCGACACCTTTAATGTAAGCACATTTATTT | 2761 GAGANGAGGCCTACANGCCAAGAAACTATAANTTTACTCTTTAATTCTTACTTTGAGCC 2820 | ATACAGTGTCACCTTGTATTAACATTTGTAATGTTGTTTTACAGTTTACATCTTTCAT TCTTTTATAGCAAATCAAACGTATTAGCTTCAGAAATTTATCAGAAGTTTAACATCTTTCAT TCTTTTATAGCAAATCAAACGTATTAGCTTCAGAAATTTATCAGAAGTTCATATAAAT TCTTTTTTATAGCAAATCAAAACGTTTTTGTTAAATAAAATTAATT |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

74.6%; Score 2361; DB 12; Length 110000;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2367; Conservative 0; Mismatches 10; Indels 0; C
3564 258563: gap of 100 bp

3564 276703: contig of 18140 bp in length

2762 27603: gap of 100 bp

5804 440802: contig of 163999 bp in length.

Location/Qualifiers

1. .440802

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/mol_type="genomic DNA"

/db xref="taxon:10090"

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| 0 | 16 | CCAATAGAAGAAG | AGAGAAAGCATGAATTACAAAGGCGCTCTCCCCACTT Z |
| ~ ^ | 1390 | GICIAGACCAMAGCACCCCCCCCCCCCCCCCCCCCCCCCC | |
| _ | 1450 | rcaacerrererer | AAT 150 |
| 0 | 04 | rcaaccircrircicr | ATAGAGACCAAAACATCAGACTTGGATAAGTAAAAT 209 |
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| | ~4 | CTTGTTCCTATCCATGATAGCCA | 0 1 |
| 0 | | CTTGTTCCTATCCATGATAGCC | |
| ~ 0 | 1630 20863 | TIGIGCCAAAGACCCITICIGA | AGANTGECTGAANTCATGGGCGAATTTTAACACA 1889 BAGAATGTCTGAATCATGCGCCGAGTTTTTACACACA 20804 |
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| _ | 1810 | CAGTTCGCTTGTGACATTAAGCT | σ |
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| ~ 0 | 1870 | CTTCTTTGTCTATATTTTCCTT | ACCTITATCAGATTGTATTCGAGCTTCCTGCTTTGGG 1929 |
| _ | 193 | 95 | PACAGGATCAACTCAATGACATAAAGTAGTTCAAACA 1989 |
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| ~ 0 | 2050 | GAACATCTACTTGATATCAGACO | TACTIGATATCAGACGGAGGACCATCCTCCATTGGAGAATATGAAGATAT. 2109 |
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| 0 | 20383 | CACTGO | GCCATTAATTGATAAGATACCACAAGCATCATCATG 20324 |
| 5. | 217 | CCAGTTATGAACACAGTGCTGAA | |
| 0 | 323 | ccagriardacacagrecrear | GGATCATAGACAGGGGGGGTTAAATCTGATCCCAGT 202 |
| > . | 2230 | AGAATAAACTTCAGTGTACCTAT | TCAGGGAAGAGTTAATTTCACAATTAAAACTAGTAA 2289 |
| 0 | 263 | AGAATAAACTTCAGTGTACCTAT | |
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| , , | 235 | . 2 | 240 |
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| | 1030 ATACCGCTTGTCACAGGCTTG TGATTGCAAGTGTCGCTGTGGAAACTGTGAAAACGT 1089 | 1150 CTACTATGATAACATGTTACCT | 1270 TTAACGTTTCTTAGAAGAGAAA HATTTCAGGAGGTGGAGTGGATGTGTCACAGCATCT 1329 | 1390 GTCTAGACCAAAGCCACCGCCCCCCCCCACCACCACCACCACCA | 1510 GAGATAATTTTCAAATCATCA AGAATTTGATTTGACCAGGGTCTCTCAGAATGCTTC | BAGAATGTCTGAATCATGCGCCGAGTTTTTACACACA | 1810 CAGTTCGCTTGTGACATTAAGC 5GGTTGGGGTTTTGGTGGGTTTTGGGGGGTTTCTTCA 1869 37780 CAGTTCGCTGACATTAAGC 5GGTTGGGGGTTTTGGTTGTTTGTTTTGTTTTTGTTTTTGTTTT |
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| 6 B 6 B 6 B 6 B 6 B | | Db Oy Oy Oy Bb Bb BX32542 WPCOMMEN Sequen Sequen BX33 BX33 BX33 BX33 BX33 BX33 BX33 BX3 | 3070 AGGGTAAAAGGCTTTTTGTTAA TAAAATAAAATTTATTATTTTTTTTTT | GAATAGA 39039 CAACATT 3129 CAACATT 39099 2 |
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| a & a | 38200 AGAATAAACTICAGIGIACCTATITCAGGGAAGAGITAATITCACAATIAAAACTAGIAA 38259 2290 AIGAACCAAITCTIAGGCACAITAAGIGGATICTGAGIAAAAGAAAGGGAACAGGGAA 2349 38260 AIGAACCAAITCTIAGGCACAITAAGIGGATICTGAGIAAAAGAAGAGAAAGAGAAGAG | Continue Query Best I Matche | <pre>httion (3 of 5) of BX322642 from base 200001 (BX322642 Mus Match Adatch Accal Similarity 99.6%; Prof. No. 0; se 2367; Conservative 0; Assmatches 10; Indels</pre> | musculus chromosome 2 (1000; 0, Gaps 0; |
| දු දු | 2350 AAAGCTGTTCGCTTCGTTCTGATTACCCAAATGAGCATGCTGGAAGGAGGTTGTGAGGCT 2409 11 | ζ. Op | 790 CATTATAACCTGAAGTACCAGAATTGAAGGAGAAGAAAGCACAGTTTTGGAGGACAT | AGGACAT 849 |
| දු පු | 2410 AGGCTAAAACCTCTGCGTAGGGAGAGAGTACAGTGCATGAGTGTGGCGGCGTTTTGTCCAC 2469 | % q | 850 CTCCACCTÀTGGAGATGCATTCCTCCTGCCAGCATTTTCCTATCGGGCCAACACAGG | acacagg 909 acacagg 98387 |
| දු පු | 2470 ACTCGTGAAGGGTGAGTAATTCAGAGCCAATCACATCAC | % q | 910 CAICTCTTTAAAGTCTACCAAA CACTCAAAGAGTCAAAAATGAGGCAAAAGGTTCTCT | GGTTCTCTT 969 GGTTCTCTT 98327 |
| දු පු | 2530 ATCACTTCAGGGGGGAGATGAATGCTTTCATGAGAAATTACACTCATAAGCTAAGCATCAG 2589 - | or or | 970 CTTCCATCCCAGGTACCTGAGA ACCTCGCTCTTTCTGGAGAACTAAAGGGGTGACTGC | TGACTGC 1029 TGACTGC 98267 |
| 중 옵 | 2590 ITTIGAGIAAAAITIGAGIAGAIGITAAAITGAACAITITIAIACCICTIACUAAIGICC 2649 | ço Op | 1030 ATACCGCTTGTCCACAGGCTTGATGCAAGTGTCGCTGTGGAACTGTGTAAACGT | AAAACGT 1089 AAAACGT 98207 |
| දු පු | 2650 CACCGACACCTITTAANGTAAGACATTTATTTAAGTTACTTGACATTAAATGCTA 2709 | \$ 60 60 | 1090 GAAGCTCTÀCGGATTCTGGCCTTTCTAAGACTATCGAAGACACCCCACTCAGTCACCACTAGACACACAC | GTCACCA 1149 GTCACCA 98147 |
| දු පු | 2710 IGICTGTATATICTGTICATCCATCGATTTTCCCAAAAGTAAGAGGAGAGAGAGAGG 2769 | \$ G | 1150 CTACTATGATAACATGTTACCTAAGGTTTCCACAGATGCCTAAAGAATACAGCAA | ACAGCCA 1209 |
| දු දු | 2770 CCTACANGCCAAGAAAACTATAAATTTTACTCTTTAATTCTTAGAGCCAGCTTGTIG 2829 | oy Op | 1210 AATGCTCCAGCTCCATATGAGAGSAATCCTCAAACTGCAATTCAGCAAATGTGAAACGGC | AAACGGC 1269 |
| & a | 2830 ITTATCAAGTGCTTTTTTGAAGAGACACCCCTGTGAATTCTTCATTCTGATACAGTGT 2889 38800 ITTATCAAGTGCTTTTTTGAAGAGACAGCACCCTGTGAATTCTTCATTCTGATACAGTGT 38859 | රු දැ | 1270 TTAACGTTTCTTAGAAGAGAA ATTTCAGAGGTGGAGTGGA | GCATCTC 1329 GCATCTC 97967 |
| රු සි | 2890 CACCTTGTATTTAACATTTGTAATGTTGTAGTTTACATCTTTCTT | ò a | 1330 CADADAGCCAATAGAAGGAGGG TAGAGADAGCATGAATTACAAAGGGGGTCTCCCACTT | CCCACTT 1389 CCCACTT 97907 |
| දු පු | 2950 GCAAATCAAAGGTATTAGCTTCAGAAATTTATCAGAAGTTCATATATAATATTTGCAA 3009 | ò a | 1390 GICTAGACCACAGACCCCCCCCCCCCCCCCCTTAGAGCCTCCACGAGTCACTCATTCTC | CATTCTC 1449 CATTCTC 97847 |
| È | 3010 AGGGTAAAAGGCTTTTTTGTTAAATAAAATTAAATTTATTT | ò | 1450 ACCTTCAACGTTCTTTCTCTGAGATAGAACCAAAACATCAGACTTGGATAAGTAAAAT | STAAAAT 1509 |

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Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., pixed quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the chone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

EMBL; SW:, SMISSEROT; TT:, TREMBL; WD:, WORMPEP; information of the WORWPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130509 CTTTTAATTCGGCAGGTACCAGAATTTGAAGGAGAAGAAAGCACACAGTTTTTGGAGGACAT 130450
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from the RPCI-23 Mouse BAC Library
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                                                                                                                                                                                                                                                                                                        constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6.
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                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/db_xref="taxon:10090"
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/clone="RP23-185P20"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Ly, Carroll, L., De Anda, C., Dederich, D.,
Lamo, C., Ding, Y., Dinh, H., Divya, K.,
Ly, Dunn, A., Durbin, K., Duval, B., Eavee, K.,
Ly, Eangle, C. R., Falls, T., Fanger, P.,
Rills, R., Garda, M., Gaerra, M.,
Gill, R., Garda, M., Gaerra, W., Garta, M.,
Hamil, C., Hamilton, C., Hamilton, K.,
Hamil, C., Hamilton, K.,
Hamil, C., Hamilton, K.,
Hamil, C., Hamilton, K.,
Jadun, S.L., Hodgson, A., Hogues, M.,
Jadun, S.L., Hodgson, A., Hogues, M.,
Jadun, S.L., Hodgson, A., Hogues, M.,
July, S., Khan, Z., King, L., Kovar, C.,
July, S., Khan, Z., King, L., Kovar, C.,
Ondon, P., Longacre, S., Lopez, J.,
Je, M., Markin, R., Marling, K., Mangum, A.,
Jarin, K., Markin, R., Marking, E.,
McNeill, T. Z., Meenen, E.,
McNeill, T. Z., Meenen, E.,
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Moris,S., Munidasa,M., Murphy,M., Nair,L.,
Naton,N. Nguyen,N., Noris,S.,
Naton,N., Nguyen,N., Noris,S.,
Naton,Perez,L., Pfannkoch,C.,
Pez,A., Perez,L., Pfannkoch,C.,
Perez,L., Pfannkoch,C.,
Parez,R., Reeves,K., Regier,M.A., Reigh,R.,
Re Y., Reuter,M., Rose,R., Ruiz,S.J.,
S. Herer,M., Rose,R., Ruiz,S.J.,
S. Herer,S., Scott,G., Shatsman,S., Shen,H.,
S. Stason,I., Sitter,C.D., Smajs,D.,
Cong,X.-Z., Sortelle,R., Soasa,J.,
S. Tingey,A., Trejos,Z., Usmani,K.,
Thmas,S., Tingey,A., Trejos,Z., Usmani,K.,
Marsen,R., Weden,H., Wotley,K.,
M.J., Warren,R., Wei,X., White,F.,
M.J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
J. Zhou,X., Zhao,S., Dunn,D., yon
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77030, USA
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Cleveland, C., Cockrell, R.,
Davila, M.L., Davis, C., Drygado, O., Dengon, S., Dragan-Rocha, S.
Bran, A., Escotto, M., Eugne
Fernandez, S., Finley, M., Fugene
Fernandez, S., Finley, M., Eugne
Fernandez, R., Harlak, P., Hadand, W.,
Harvey, Y., Havlak, P., Hadand, W.,
Jackson, L., Jacob, L., Jing,
Jackson, L., Kelly, S., M.
Hollins, B., Meylls, S., K.
Ilu, J., Liu, W., Liu, Y.,
Ilu, J., Liu, W., Liu, Y.,
Indrawheshwari, M., Mahindart e,
Mangum, B., Mapua, P., Marindart e,
Mangum, B., Mangua, P., Marindar, M.,
Nackelemeh, O., Okwuonu, V.,
Patend, M., Savery, G., She
Shetty, J., Shvartsbeyn, A,
Shetty, J., Shvartsbeyn, A,
Sneed, A., Sodergren, E.,
Shetty, J., Shvartsbeyn, A,
Sneed, A., Schery, G., Steimle, M., Strong, R.,
Wright, D., Wright, R., Wu, J.
Wright, D., Wright, R., Wu, J.
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Weinstock, G. and Gibbs, R.
Direct Submission
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Submitted (19-NOV-2002)
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Direct Submission
Submitted (09-MAY-2002)
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Rattus norvegicus clone CH230-65J6, WORKING DRAFT SEQUENCE, 2
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Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Angulabechi, V., Allen, C., Aoyadi, A., Aydodi, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buyar, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, G., Chen, Y., Chen, Z., Chu, J.,
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
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AC120773.5 G1:25082599
HTG2 PHASE1; HTGS_PULTOP.
Rattus norvegicus (Norway rat)
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ò 요 ò 셤 VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION

RESULT 6 AC120773

ACCESSION

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                                       IGGATGTCTCACAGCATCTCCAAAAAGCCAATAGAA
                                                                                                                                           GCACAAGAGCTCCCCGACTTGGCTAGACCAAAGCCC
                                                                                                                                                                                                                        ITATCAGACTCCGACAAGTAAATGAGATCATGTTTA
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                                                                                                                    ACAAAGGCGCTCTCCCACTTGTCTAGACCAAAGC--
                                                                                                                                                                                                 GCCTCCACGAGTCACTCATTCTCACCTTCAACGTTC
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                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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shows, Andrews, Bloke, Barber, M., Barnetead, M., Benahmed, F., Blum, F., Blyth, P., Brown, M., Benahmed, F., Blyth, P., Brown, M., Benahmed, F., Brown, M., Grand, C., Cener, A., D'Souza, L., R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Porano, C., Ding, Y., Dinh, H., Divya, K., Dunn, A., Durbin, K., Duval, B., Rawes, K., S., Dunn, A., Durbin, K., Duval, B., Rawes, K., S., Bunn, A., Durbin, K., Duval, B., Garza, M., Gall, K., Garcia, A., Hogeson, A., Hogues, M., Gall, K., Cardo, M., Hornandez, J., Ladwil, S., Khan, Z., King, L., Kovar, C., Gow, H., Johnson, B., Johnson, R., Johnson, R., Johnson, R., Lozado, R.J., Lu, Z., Liu, J., Chi, M., Martin, R., Martin, R., Martinez, E., Monen, E., McNeill, T. Z., Menen, E., McNeill, T. Z., Martinez, E., Marti

Fernandez, B., Finley, M., Fraser, C.M., Gabisi, A., Gebregoorgis, E., Geer, K. Gunaratne, P. Haaland, W. Harvey, Y., Havlak, P., Harenandez, R., Hines, S.,

, Escotto, M., Eug

Karpathy, S., Kelly, S., K L Kowis, C., Kraft, C.L., Le Liu, J., Liu, W., Liu, Y., Loulsege, L., Loulsege, Maheshwari, M., Mahindart,

Hollins, B., Howells, S., Jackson, L., Jacob, L., Ji

Biswalo, K., Blair, J., Bl. h Bryant, N., Buhay, C., Bur h, Cardenas, V., Carter, K., a, Chacko, J., Chavez, D., Ch. d. Cleveland, C., Cockrell, R. Davila, M.L., Davis, C., Dry Delgado, O., Denson, S., Drz Draper, H., Dugan-Rocha, S.

| REFERENCE AUTHORS | | | | TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL | REFERENCE AUTHORS |
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| 2329 AAAGAAAGGGAACAGGAGAAAGCTGTTCGCTTGGTTTCCGAAATGA | 2444 GCATGAGTGGGGGC-TTTTGTCCACTCGTGAAGGTGAGTAATTCAGAGCCAA 2499 [2414 GCATGAGTGGGGGC-TTTTGTCCACACTCGTGAAGGTGAGTAATTCAGAGCCAA 2499 [25236 GCATGGGGGGTGGTTTTTGTCCACACTCGTAATTCAGTGGTTATTTTGTCAA 2599 2500 TCACATCACAGGATGGACACCCTAACTCACTCACTCATTCAGGGGAATGA 2549 [1 | 2610 GAIGITAMATATGAACATTTTATACCTCTTACTAATGTCCCCCCCACCCTTTTAATGTA 2669 | 2789 ATAAATTTTACTCTTTAATTCTTACTGAGCCAGCTGTTGTTATCAAGGCTTTTTTG 2848 [| TTAAATAAAATAAAA | 59946 CCACTATTIGCAAAGAAA 59963 |
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Mindlas, Montemayor, J., Moore, S., Mindlass, M., Murphy, M., Nair, L., Nethon, N., Norris, S., Munidasa, M., Murphy, M., Nair, L., Nethon, N., Norris, S., Parks, K., Perez, A., Perez, L., Pfannkoch, C., Perez, A., Perez, L., Pfannkoch, C., Popovic, D., Primus, E., Pul, L.-L., Reigh, R., Rose, M., Rose, R., Ruiz, S.J., Shen, H., Sher, S., Scott, G., Shatman, S., Shen, H., Sisson, I., Sitter, C.D., Smajs, D., Sten, R., Sorelle, R., Sosa, J., Sten, R., Sten, R., Trejos, Z., Usmani, K., Mana, D., Waldron, L., Walker, B., Wang, J., Marren, R., Wei, X., White, F., Marren, R., Wei, X., White, F., Marren, R., Wei, X., White, F., Wakub, S., Yen, J., Yoon, L., Yoon, V., Zhao, S., Dunn, D., von, Smith, D.R., Smith, H.O., edu/projects/rat/). Each contig described represents a scaffold in the Atlas dd). Within each contig scaffold, ls are ordered and oriented, and separated uman Genome Sequencing Center, Department netics, Baylor College of Medicine, One 77030, USA mman Genome Sequencing Center, Department netics, Baylor College of Medicine, One 77030, USA nnce version replaced gi:24819385.

Liby is a combination of BAC based reads equencing reads assembled using Atlas sortium. Mangum, B., Mapua, P., Mar II Mawhiney, S., McLeod, M. P. N Milosavijevic, A., Miner, Morgan, M., Morris, K., Mo Nankervis, C., Neal, D., N Nwaokelemeh, O., Okunoun, Pasternak, S., Paul, H., Pre Plopper, F., Poindexter, A Steimle, M.; Strong, R., S. Taylor, T., Thomas, N., Thomas, N., Thomas, N., Thomas, N., Thomas, N., Valla by Wang, Q., Warren J., Waright, D., Wright, R., Yu, F., Zhang, J., Zhou, J. Puazo, M., Quiroz, J., Rac L Reilly, B., Reilly, M., Re, Rives, C., Rodkey, T., Roj s Sanders, W., Savery, G., So Shetty, J., Shvartsbeyn, A., Sneed, A., Sodergren, E., Baylor Plara, Houston, T. On May 10, 2003 this sequence in this ass and whole genome shotgun (http://www.hgsc.bcm.tmc of Molecular and Human G Baylor Plaza, Houston, T 3 (bases 1 to 264245) Rat Genome Sequencing Co. Yu,F., Zhang,J., Zhou,J., Niederhausern,A., Weiss,I Weinstock,G. and Gibbs,R Direct Submission of Molecular and Human G assembly (a 'contig-scafindividual sequence cont in the feature table bel assembly (a 'contig-scaf Direct Submission Submitted (28-SEP-2001) Direct Submission Submitted (10-MAY-2003) (bases 1 to 264245) Unpublished Worley, K.C. EFERENCE AUTHORS TITLE JOURNAL TITLE JOURNAL EFERENCE AUTHORS TITLE COMMENT

AC096804 264245 bp DNA linear HTG 10-MAY-2003
Rattus norvegicus clone CH230-44K10, *** SEQUENCING IN PROGRESS
***, 2 unordered pieces.

RESULT 7 AC096804/c LOCUS

DEFINITION

AC096804.6 GI:30521409

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Page 12

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                                                                                                                                                              Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help&bcm.tmc.edu

Contact: hgsc-help&bcm.tmc.edu

Center project Information
Center clone name: GFPQ

Center clone name: GFPQ

Center clone name: GFPQ

Center clone name: GFPQ

Consensus quality: 215957 bases at least Q40

Consensus quality: 225988 bases at least Q30

Consensus quality: 225088 bases at least Q30
by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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8879 262978: gap of unknown length
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//organism="Rattus norvegicus"
//mol_type="genomic DNA"
//db_xref="taxon:10116"
//clone="CH230-44K10"
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clone_end:T7
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| TAAATTATCTCCTAGCAACATTGGTCACGTTTCAATC 3144 | 197 bp mRNA linear ROD 11-JUL-2005 r alpha-2,8-sialyltransferase (SIAT8F ase, ST8Sia-VI. | rat) ata; Craniata; Vertebrata; Euteleostomi; hontoglires; Glires; Rodentia; uridae; Murinae; Rattus. one,R., Delannoy,P. and Oriol,R. ases and slalyltransferase-related genes: | riol R., U504, Inserm, 16 Av. Paul , FRANCE ers s norvegicus" | 00= | 2,8-sialyltransferase" 2,8-sialyltransferase" 2,8-sials: 2xC7" 2xC7" 7::IPR01675" FXB/TYEMBL:Q6ZXC7" | M. PGGTIFATUSELLITAL PROPADAPAS NALGEBS REET T. VPRTRNSTYLDEKTPETAEKCKGLKYSLDSLANKTRRYSEDD CR. AESTENFRAKLASCCDALODFVVSQNNTPVGSNMTYEVESKK SPFVDY PYNQCAVVGNGGILNKSLCGAEIDKSDFVFRCNLPPI JV. WNPSI ITLKYKNLAEKKARFLEDIS AX VGDAFLLLEAFSYRVN SK. RQXVL FFHPRYLALFRATKGVTAYRLSTGLMAAS IAVEL CTT BEIPLSHHYYDNKLPKHGFHQMPKEYSQMLQLHMKGILKLQF | re 1028; DB 6; Length 1197; d. No. 0; Mismatches 105; Indels 0; Gaps 0; GCCCTCATAGGCAGCCTGATGCTGCTCCTCCTG 136 [|
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| Oy 3085 CTGCTAATGAACCTAATTAGCT | 23 AJ699423 TION Rattus norvegicus mRNA figene). ION AJ699423.1 GI:47057304 N AJ699423.1 GI:47057304 DS galpha-2,8-sialyltransfe | M Rattus norvegicus (Norwa Rattus norvegicus Eukaryota; Metazoa; Chor Mammalia; Eutheria; Euar Sciurognathi; Muroidea; 1 Harduin-Lepers,A., Molli The animal, stalyltransfe a phylogenetic approach Glycobiology 15 (8), 805 | PUBMED 15843597 REFERENCE 2 (bases 1 to 1197) AUTHORS Oriol, R. TITLE Direct Submission JOURNAL Submitted (104-MAY-2004) Vaillant-Couturier, 9480 FEATURES Liccation/Qualif source J., 1197 Authory | /mol_type="mRNA" /grain="Spragu" /db xref="taxon /clone="ST8Sia-" gene 11197 CDS 11197 CDS 11197 /gene="SIAT8F" | / codon etart=1 / product="alpha / product="lalpha / product=1 id="CA / db_xref="GOA:0 / db_xref="GOA:0 / db_xref="Inter" / db_xref="Inter" | /translation=' GGTSAALKTLWSPY YLOIVTNICRCPW YLOIPTRENIFHMFPY TGSASQOVGSKTNI TGISFKVYQTLKES CENVTLYGFWPFSS SKCBAA" | Query Match Query Match Best Local Similarity 91.2%; Pr Matches 1091; Conservative 0; Qy 77 ATGAGATCGGGGGCACGCTGT |
| 246305 AGTAGTTCCAGTATCTGCTACTTCTCACAGGTTATCATATCCAGGAAGTTACCGGCCGA 246246 2034TITTATTTAAAATAGTGAACATCTACTTGATATCAGACCCGAGGACCATCCTCCATTG 2091 [| | TITCACAAITAAAACTAGAAATCAAITCTTAGGCACAITAGGCAAITCTGAGIA TITCACAAITAAAACTAGAAAACGAATTCTTA-GCAAGTTAAGTGGATTCTGAGIA TITCACAAITAAAACTAGAAAACGAATTCTTA-GCAAGTTAAGTGGATTCGGGGTA AAAGAAAGGGAACAGGAGAAAACTGTTCGCTTGGTTCTGATTACCCAATGA AAAAAAAAAA | 245893 GTATGCTGATAGTAGACTGTGAGGTTGCCTGACACTCTGTGTTAGGAGAGAGA | AIGCITTCAIGAGAAATTACACTCAIAAGCTAAGCATCAGTTTTGAGTAAAATTTGAGTA ACGITTTCAIGAAAAATTGCACTCAITGGCTAAGCATCAGTTTTGAGTAAAATTTGAATA GATGTTAAATATGAACATTTTATACCTCTTACTAATGTCCCACCGACACCTTTTTAATGTA | | | 2909 GTAATGITICAAGITTACATCITCITCATTTATAGCAATCAATCAATCAGC 2968 245360 GTAACGTGTCAAGITTGCTTCTTTTATAGCCAATCAACGTATTAGC 2968 2969 TTCAGAAATTATCAGAAGTTCATATAAATTTTGCAAAGGGTAAAAAGGCTTTTTG 3028 245303 TTTAGAAATTATCAGAAGTTCATATAAATTTTGCAAAGGGTAAAAAGGCTTTTTTG 245244 3029 TTAAATAAAATAAAATTTATTATTTCTTCTGATGAATACAGGCTCTTTTATGCTG 3084 245243 TTAAATAAAATAAAATTTATTATTTCTTCTGGTGAATACAGGCTCTTTTATGCTG 3084 245243 TTAAATAAAATCAAATGTATTATTATCTTCTGGTGAATACAGGCTCTTTTATGCTG 3084 |

| 13 And a control of the control | 1141 CAGCTCCATATGAAAGGGATCC CAAACTGCAGTTCAGCAAATGTGAAGCCGCTTA 1196 | AJ621583 A24 bp mRNA linear PRI 11-JUL-2005 Homo sapiens partial mRNE for alpha2,8-sialyltransferase (ST8SIA VI | 583 583.1 GI:46517895 78.8431V1 transferalb: STBSIA VI cene | ata, Craniata | Molli One, R., Delannoy, P. and Oriol, R. | | Parduin-Lepers A., | Lille 1, Unk Ciks USIL nds/b, villeneuve d'Ascq. Location/Qualif ers 1, 1234 /organism="Homo Bapiens" | / wo.refe="mkNA" / db_xrefe="nexon 9606" / chromosome="10" / map="10pl2.31" | - ق | <pre>/direction="State" /function="state" acid transfer" /function="state" acid transfer" /functional details</pre> | recolugation reco | /db_xref="GOA:PUG47" /db_xref="GOA:PUG47" /db_xref="UnlPrc.KB/Swiss-Prot:P61647" /translation="MPGGALALLALLILLILLIMCPADAPGRARILVEESREAT | HGITHALKTUREPERTUPERTATION STILLEREN SALGUIEREN MED ELES FENNT INGSEEND YLOTHINGSCPRERGERANDERAKLASCCDAVONFVVSONNTPVGTINNSTREKEK ETPEKNIFHMEPVSC. PFVDYPTNQCAVVGNGGILNKSLCGTEIDKSDFVFRCNLPPT TGDYSKNYGSKYNTANT THESTILLEKKGNALEKKRALEELEDIATVGDAFFLLASFSFRAN MEMORYANYANT STAFFANTANT THESTILLEKKRALEKKRALEEDIATVGDAFFLLASFSFRAN | SKCEVA" SKCEVA" | tch al Similarity 82.0%; Prd. No. 3.9e-271; 1006; Conseivative 0; dismatches 217; Indels 4; Gaps 1; | 77 ATGAGATCGGGGGGCACGCTGTT CGCCCTCATAGGCAGCCTGATGCTGCTGCTCCTCCTG 136 | 137 CGTATGCT-CTGCTCCCGCTGCCCGCTCCAGGCTGTTGATGCAGGAAGC 196 | 197 AGAGAGGACCCAGTGGTACCTGAGCACTGAAGACACTCTGAAGCCCGACAACCCCG 256 |
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| AGGGCAGGCCCCAGCCCCAGCCCCCCCCCCCCCCCCCC | | RESULT 9 AJ621583 LOCUS DEFINITION | ACCESSION VERSION KEYWORDS | SOURCE | REFERENCE AUTHORS | JOURNAL | REFERENCE AUTHORS TITLE JOURNAL | FEATURES BOUICE | | gene | S | | | | ORIGIN | | | | |
| AGGGCAGGCCCCAGCCCCAGCCCCCCCCCCCCCCCCCC | | | | | | | | | | | | | | | | | | | |
| | AAAGC | agagaggacaccagtgctacctcagctgcactgaagacactctggagcccgacaaccccg | GTACCACGCACCAGGAACAGCACATATCTGGATCAGAAGACAACCCAAATAACAGAAAA | TGCAAAGATCTGCAATATAGCTTGAACTCTTTATCTAACAAAACGAGACGGTACTCTGAG | GATGACTACCTCCGGACCATCACAAACATACAGAGATGCCCATGGAACCGGCAAGCAGAAA | GAATATGACAATTTAGAGCAAAACTGGCTTCCTGTTGGGATGCCATTCAAGACTTCGTG | GTTTCCCAGAACAACACTCCAGTGGGGACTAACATGAGCTACGAGGTGGAAAGCAAGAAA | CACATCCCCATTCGAGAGAACATTTTCCACATGTTTCCAGTGTCGCAGCCTTTTGTGGACCTATTTCTGTGACCCATTCCAGTGTCCCCATTCGAGAGAACATTTTCCACATGTTTCCAGTGTCAGAGAGACACTTTTGTGGAC | TATCCCTATAACCAGTGGGCAGTGGTTGGTAATGGGGGAATTGTCAACAAGAGTGTCTCTGG | GGAGCAGAAATHGATAAATCTGACTTCGTCTTCAGGTGTAACCTCCCCCCAATCACAGGGGGGGG | AGCGCTAGTAAAGATGTTGGAAGCAAACCAATCTTGTGACTGTCCAGATCTTATA | acctgaagtaccagaatttgaaggagaagaaagcacagtttttggaggacatctccacc | TATGGAGATGCATTCCTCCTCCTGCCAGCATTTTCCTATCGGGCCAACACAGGCATCTCT | TTTAAAGTCTACCAAACACTCAAAGAGTCAAAATGAGGGAAAAGGTTCTCTTCTTCCAT | CCCAGGTACCTGAGACACCTCGCTCTTTTCTGGAGAACTAAAGGGGTGACTGCATACCGC | TIGICCACAGGCTIGAIGAITIGCAAGTGTCGCTGTGGAACTGTGTGAAAACGTGAAGCTC | TACGGATTCTGGCCTTTCTCTAAGACTATCGAAGACACCCCACTCAGTCACCACTACTAT | GATAACATGTTACCTAAGCATGGTTTCCACCAGATGCCTAAAGAATACAGCCAAATGCTC | cagctccatatgagaggaatcctcaagctgcaattcagcaatgtgaaacggctta |

| 197 bp mRNA linear PRI 11-JUL-2005 ralpha-2,8-sialyltransferase 8F (siat8F se 8E, siat8E gene. | ata; Craniata; Vertebrata; Euteleostomi; hontoglires; Primates; Catarrhini; one,R., Delannoy,P. and Oriol,R. ases and sialyltransferase-related genes: 817 (2005) | riol R., U504, Inserm, 16 Av. Paul , FRANCE ers roglodytes" | sialic acid to another sialic acid" 12,8-sialyltransferase 8F" 126901.1" 1648" | LKB/Swiss-Prof:P61648" PGGALLALLALLILLILLINLWCPADAPGRATILVEESREAT PGGALLALLASLALLILLINLWCPADAPGRATILVEESREAT PROPATWSTYLMEKSLHUTEKCKNLOYGI ESPENKTKGYSEND AEBYANFRAKLASCCDAVQNFVVSQNNT PVGTNMSYEVESKK PPVDYPYNQCAVVGNGGILANSLCGFEI DKSDFVFRCNLPPT INPSIITLKYGNIKEKKALLEDIATYGEAFFLLPPST ROKYLPFHPKYLKOLALFWRYKGVTATRLSTGAMITSVAVEL EDIPVSHHYYDNKLPKHGFHQMPKEYSQILQLHMKGILKLQF | re 857.8; DB 5; Length 1197; d. No. 8e-270; Mismatches 212; Indels 0; Gaps 0; CGCCTCATAGGCAGCCTGATGCTGCTCCTCCTC 136 | CGGCCCGGCCGCCATTCTGGTGGAGGAAAGC 120 AGTGCACTGAAGCATCTGGAGGAAAGC 120 AGTGCACCGCGCGCGCGACCCCG 256 |
|---|---|--|---|---|--|---|
| RESULT 10 AJ697663 LOCUS DEFINITION Pan troglodytes mRNA for gene). ACCESSION AJ697663.1 GI:46517916 KEYWORDS alpha-2.8-sialyltransfer SOURCE Pan troglodytes (chimpan ORGANISM Pan troglodytes | EUKARYOCIA; Metazoa; Chor Mammalia; Butheria; Euar Hominidae; Pan. REFERENCE 1 AUTHORS Harduin-Lepers, A., Molli TITLE The animal sialyltransfe a phylogenetic approach JOURNAL Glycobiology 15 (8), 805 REFERENCE 2 (bases 1 to 1197) | Direct Substituted Vaillant-ted Vaillant-ted Cee 1 | CDS 111197 /gene="statep" /function=adds /codon_state=1 /product="alpha /product="alpha /product="alpha /product="alpha /product="alpha /product="alpha /product="alpha | /db.xref="Unipr" /translation="M HGTPAALRTLESPAT HGTPAALRTLESPAT STOTITDIOSCPWKR BIPIKKNIFHWFPVS TGDVSKOVGSKTNLV TGTSFKYYYTLESSKT SKCEVA* SKCEVA* | Ouery Match Query Match Best Local Similarity 82.3%; Pr Matches 985; Conservative 0; Qy 77 ATGAGATCGGGGGCACGCTGT Db 1 ATGCGCCGGGGGGCACTGC Qy 137 CGTATGCTCTGGTGCCCG | Db 61 |
| 121 | 301 AACGACTACCTTCAGATTATCACAGATATACAGAGTTGTCCATGGAAACGGCAAGCAGAA 360 437 GAATATGACAATTATCACAAACTGGCTTCCTGTTGCGATGCCATTCAAGACTTCGTG 496 | | AGGGTAGTAAAGATGTTGGAAGCAAAACAATCTTGTGACTGTCAATCCCAGCATTATA [| | CCCAAGTACCTGAAACACTTCCCTTTTCTGGAAACTAAAGGTGTGAATGCGCCCCAAGAACTTCTGGAAAACTAAAGGTGTGAATGCGCCCCCAAGAACTTATCTGGAAAACTAAAAGTGTGAAAACTGCAAAACTGCCACAGGCTTGAAAAACTGTGTGAAAAATGTGAAAACTGTGTGAAAAATGTGAAGCTGTGAAAAATGTGAAAACTGTGTGTAAAAATGTGAAGCTGTGAAAAATGTGAAGAACTGTGTGTG | |

| tra; Craniata; Vertebrata; Buteleostomi; siatheria; Cetartiodactyla; Ruminantia; Bos. Doe,R., Delannoy,P. and Oriol,R. ases and sialyltransferase-related genes: B17 (2005) arduin-Lepers A., Universite de Lille 1, 5, Villeneuve d'Ascq, 59655, FRANCE Brs | W E WWW Z H H D G G Z G G M M | re 757, DB 14; Length 1197; M. No. 1.3e-236; Mismatches 275; Indels 0; Gaps 0; DGCCCTGATAGGGAGCTGATGCTGCTCCTCTG 136 CHILL | AAACATACAGAATGCCCATGGAACCGGCAAGCAGAA 436 |
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| ORGANISM Bos taurus; Eukaryota; Metazoa; Chor Mammalia; Eutheria; Laur Pecora; Bovidae; Bovinae 1 TITLE 1 Harduin-Lepers, A., Molli TITLE 7 He animal stallyltransfe a phylogenetic approach JOURNAL Glycobiology 15 (8), 805 PUBMED 1843597 REFERENCE 2 (bases it o 1197) AUTHOR Harduin-Lepers, A. TITLE Direct Submission JOURNAL Submitted (13-DE-2004) UGSF, UMR CRRS USTL no85 FEATURES Location/Qualif Source 1199 | mol_type="mRNA mol_type="mRNA mol_type="mRNA mol_type="mRNA mol_type="mena mol_type="mena mol_type="mena mol_type="mena mol_type="mena moltype="mena mol | Ouery Match Best Local Similarity 77.0%; Pr Matches 922; Conservative 0; Oy 77 ATGAGATCGGGGGGCACGTTT Db 137 CGTATGCTCTGGTGCCACTGT OY 137 CGTATGCTCTGGTGCCACGCG OY 137 CGTATGCTCTGGTGCCACGCG OY 197 AGAGAGGAGACCGCG OY 197 AGAGAGGACACCGCG OY 257 GTACCACGCACCACCAGCGC OY 257 GTACCACGCACCAGCAGCA OY 257 GTACCACGCACCAGCAGCA OY 257 GTACCACGCACGGGAACAGCA OY 257 GTACCACGCACGGGAACAGCACCACACAGCACACACACAC | OY 377 GATGACTACCTCCAGACCATCA 11 |
| | 617 TATCCCTATAACCAGTGGGGGGGTATTCTCAACAACTCTCTGGGGGGATTCTCAACAAGTCTCTCTGGTATTCTCAACAAGTCTCTCTGGTATTCTCAACAAGTCTCTCTGGTATTCTCAACAAGTCTCTCTGGTATTCTCAACAAGTCTCTCTGGTGTATTCTCAATTCTCAACAAGTCTCTCTGGTGTATTCTCAATTCTCTAACAAGTCTCTCTTCTGGGGGGAATTCTCAACAAGTCTCTCTTGGGGGGAATTCTCAACAAGTCTCTCTTGTGGGGGGAATTCTCAACAAGTCTCTCTTTTAAGTCTAAAATTCAAAAATCCAACCAA | 11 1 1 1 1 1 1 1 1 1 | LOCUS AJ868431 1197 bp mRNA linear MAM 11-UUL-2005 DEFINITION BOSE taurus partial mRNA for alpha-2,8-sialyltransferase (siat8F ACCESSION AJ868431 VERSION AJ868431.1 GI:56562214 KEYWORDS alpha-2,8-sialyltransferase; siat8F gene; ST8Sia VI. |

| | rctaaaacteragaagacatacteecearcactatrateacaacaactectaaa 1050 catgotttecaceagatgeetalagaatacageeaaatgeteeagetecatatgagagga 1234 |
|---------------------------|--|
| PERTURES Continues | Db 991 TCTAAAACTGTAGAAGATAC Qy 1175 CATGGTTTCCACCAGATGCCTA |
| | humanexons or transcripts, for detecting expression and thereof Patent: WO 02068579-A 22613 06-SEP-2002; |

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F. .67981), complement (63443. .63555),
F. .59586), complement (56303. .57775))
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locus_tag="RP1
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Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinkton, Cambridgeshire. CB10 15A, UK. E-mail enquiries: vega@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk

On Oct 24, 2001 this sequence version replaced gi:15028618.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10
RPDI-414X1 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                ALISBIGA 151289 bp DNA linear PRI 18-MAY-2005 Human DNA sequence from clone RPI1-414K1 on chromosome 10 Contains the 3' end of the gene for the likely ortholog of mouse sialyltransferase 8-VI (alpha-2 9-sialytransferase) (STRSIA-VI), a novel gene and the 5' end of a novel gene, complete sequence. ALISBIGA 15 GI:16416157 HTG; sialyltransferase; STBSIA-VI.
1051 CATGGTTTCCATCAGATGCCCAAAGAATACAGCCAGATCCTCCAACTTCACATGAAAGGA 1110
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complement(join(<54812. .55162,57619. .57775,59494. .59586,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                  1235 ATCCTCAAACTGCAATTCAGCAAATGTGAAACGGCTTAA 1273
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Center: Wellcome Trust Sanger Institute
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/clone="RP11-414K1"
/clone_lib="RPCI-11.2"
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db_xref="taxon:9606"
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/gene="RP11-414K1.1"
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/gene="RP11-414K1.1"
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1 (bases 1 to 151289)
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.96029),

.91792,95943. .96029

iacrcaracaaarrrrraraar 57074 TGATATCAGACCGAGGACCA 2081 ---AGTTATGAACACAGTGCTG 2190 TGATTAACAATGTCTCCAAAC 57241 araaaaacarecrrrcrr 56954 raiccarregarificirrere s6897 ricrrcarcarriarrarir seese || |||| | | || ||| ||| |TCTCACTTATACGATATACTT 56599 rerrererrecererededic sesse CGAGTCACTC-ATTCTCACCT 1453 ACTTGGATAAGTAAATGAGA 1513 SGTAATGAAACTGTGCAATTGT 1633 TTAAGCTGGGTTGGGGTTTTG 1846 CATGCGCCGAGITITIACACA 1687 TITCCTTACCTTTATCAGTTT 1906 TCCCACTGACAGGATCAACTC 1966 linear VRT 11-JUL-2005 ransferase (SIAT8F gene). AGGCGCTCTCCCACTTGTCTA 1394 CCTAGTAGAGTACAG---- 1741 TGTTTTAT --- CCATAAAGTT 2023 GAAAAGCAGGTGTGTGCCATT 2139 AGAATAAACTTCAGTGTAC 2248

| ## GOOD PROPERTY IN THE PROPERTY OF THE PROPESTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPESTY OF THE PROPES | TGACTTCGTCTTCAGGTGTAACCTCCCCCAATCACA 733 | Ata; Craniata; Vertebrata; Euteleostomi; thae; Galliformes; Phasianidae; "K., Brown, W.R.A., Carder, C., Chalk, S.E., M., Francis, M.D., Grafham, D.V., T., Huut, P.J., Maddison, M., McLaren, S.R., Rogers, J., Scott, C.E., Taylor, R.G., anger Institute, Hinxton, Cambridgeshire, fries: chickest@bms.umist.ac.uk anger/Sheffield/UMIST cDNA collection, anger/Sheffield/UMIST cBNA was prepared adds, normalised, and poly A-trimmed. By Blizabeth Bosch. CDNA was prepared adds, normalised, and poly A-trimmed. en ligated into the vector. Vector: e_1: EcoRI; Site_2: NotI Host: Escherichia | |
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| alpha-1,6-stalyltransferase; SINTSP gene. Gallus gallus (chicken) Actions gallus (chicken) Making gallus (chicken) Bardunines gallus (chicken) Bardunines gallus (chicken) Bardunines gallus (chicken) Bardunines gallus Chicken gallus Chicke | 674 TGCGGAGCAGAATT 598 TGTGGAGCTGAAATC 734 GGGAGCGCTAGTAAA 658 GGAGCGCTAGTAAA 794 ATAACCTGAAATAC 718 ATAGCTCAGAATAC 718 ATAGCTCAGAATAC 854 ACCTATGGAGTGCTAC 854 ACCTATGGAGTGCTAC 854 ACCTATGGAGTGCTAC 1034 CTCTTTAAAGTCTAC 1034 CGCTGTCCACAGGC 1034 CGCTGTCCACAGGC 1034 CTCTTACAGGTTCTGG 1034 CTCTACGGTTCTGGT 1034 CTCTACGGTTCTGGT 1034 CTCTACGGTTCTGGT 1034 CTCTACGGTTCTGGT 1034 CTCTACGGTTCTGGT 1034 CTCTACGGCTTCTGGT 1034 CTCTACGGCTTCTGGT 1034 CTCTACGGCTTCTGGT 1036 CTTTACGGCTTCTGGT 1037 TACGACAGCTG 1138 CTTCAGCTTCATGGT 1138 CTTCAGCTTCATGGTTCATGGTTCATGGTTCATGGTTCATGGTTCATGGTTCATGGTTCATGGTTCATGGTTCATGGTTCATGGCTTCATGGTTCATGGCTTATGGCTTATGGCTTATGGCTTATGGCTTATGGCTTATGGCTTATGGCTTATGGCTTATGGCTTATGGCTTATGGCTTATGGCTTATGGCTTATGGCTTATGGCTTATGGCTTATGGCTTATGGTT | ten bed | |
| alpha-2.8-stalyltransferase, SIATBF gene. Gallus gallus Rukascas, Chofatta; Craniata; Vertebrata; Eucele Archosautia; Aves; Weognathas; Galliformes; Phasianidae; Phasianinae; Gallus The animal stalyltransferases and stalyltransferase-relate phasianinae; Gallus The animal stalyltransferases and stalyltransferase-relate aphylogenetic approach 10340000000000000000000000000000000000 | | 433 433 443 417 553 673 597 | |
| KETWORDS SOURCE ORGANIS SOURCE TITLE TITLE TOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL TITLE COURNAL PUBMED SOURCE Gene Gene Gene Gene Gene Matches Db | alpha-2,8-sialyltransferase; SIATBF gene. Gallus gallus Gallus gallus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. Harduin-Lepers,A., Mollicone,R., Delannoy,P. and Oriol,R. The animal sialyltransferases and sialyltransferase-relate a phylogenetic approach Glycobiology 15 (8), 805-817 (2005) 15843597 2 (bases 1 to 1197) Oriol,R. Oriol,R. Direct Submission Submitted (04-MAY-2004) Oriol R., U504, Inserm, 16 Av. Pauv Vaillant-Couturier, 94807, FRANCE Location/Qualifiers Location/Qualifiers (mol type="mRNN" Abs. Tref="taxon:9031" Clone="STRBS!" 1.1197 Gene="STRBS!" 1.1197 Gene="STRBS!" 1.1197 Location-"adds sialic acid to another sialic acid function="alpha-2,8-sialyltransferase" Ab.xref="UniProtReVIPERSARCE" Ab. | GKCESD" GKCESD" 14.8%; Score 467.2; DB 11; Length 1197; cal Similarity 67.9%; Pred. No. 3.5e-141; 652; Conservative 0; Mismatches 308; Indels 0; G 314 AAAIGCAAAGATCIGCAATATAGCTIGAACTCTTATCTAACAAAAGGTAA 238 AAAIGTAAGGCAATATAGCTTCAAAACTCTTATCTAACAGAAGAAGGTAA 374 GAGGATTATTATCTTCACAACAATTTGTCATCGTCGTTCATCAGAAGGAAG | |

| cctcaactgcaattcagcaargtgaaacggcttaa 1273 | | | | | | | | | | | | | | |
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| Oy 1214 CTCCAGCTCCATATGAGGAA | | | | | | | | | | | | | | |
| <pre>## source</pre> | Query Match 14.4%; Score 456.8; DB 11; Length 1520; Best Local Similarity 67.9%; Pred. No. 9.8e-138; Matches 652; Conservative 0; Mismatches 307; Indels 1; Gaps 1; 314 AAATGCAAAGATCTCCAATATAGCTTGAACTTTTATCTAACAAAGGAGACGGTACTCT 373 | 229 AAATGTAAGGCAATTCAGGACAACATTTGTCATCGTCGTTCAAGAAGAAAAGGTATCCA 288 374 GAGGATGACTCCCAGACCATCACAAACATACAGAGATGCCCATGGAACGGCAAGCA 433 | | 408 ATTGCTTCTCAAAACAACCCCCACTGGGAAGTAACATGAGTTATGAAGTGGACAGTAAA 467 554 AAACACATCCCATTGGAGAACATTTTCCACATGTTTCCAGTGTCGCAGCCTTTTGTG 613 | 614 GACTATCCCTATAACCAGTGCAGTGGTAGTAATGGGGGAATTCTCAACAGTCTCTC 673 | 674 TGCGGAGCAGAAATTGATAAATCTGACTTCGTCTTCAGGTGTAACCTCCCCCCAATCACA 733 | 734 GGGAGCGCTAGTAAAGAIGTIGGAAGCAAAACAAATCTIGIGACTGTCAATCCCAGCAIT 793 | 794 ATAACCCTGAAGTACCAGAATTTGAAGGAGAAAGCACAGTTTTTGGAGGACATCTCC 853 | 854 ACCTATGGAGATGCATTCCTCCTGCCAGCATTTTCCTATCGGGCCAACACAGGCATC 913 | 914 TCTTTAAAGTCTACCAAACACTCAAAGAGTCAAAAATGAGGCAAAAGGTTCTCTTCTTC 973 | 974 CATCCCAGGIACCTGAGACACCTCGTCTTTTCTGGAGAACTAAAGGGGTGACTGCATAC 1033 | 1034 CGCTTGTCCACAGGCTTGATGATTGCAAGTGTCGCTGTGGAACTGTGTGAAACGTGAAG 1093 | 1094 CTCTACGGATTCTGGGCCTTCTCTAAGACTATCGAAGACACCCCACTCAGTCACCACTAC 1153 1008 CTTTACGGCTTCTGGCCTTTCTCAAAATCCACAGAGAAGATGCCAATCAGCCACCACTAT 1067 | 1154 TATGATAACATGTTACCTAAGCATGGTTTCCACCAGATGCCTAAAGAATACAGCCAAATG 1213 |

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BI653314 603301030
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BB112539 BB112539
BB67781 BB627781
BE633149 uv73e09.
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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HIPIRRNIFHWFPVSQPPVDYPYNOCAVVGNGGILNKSLCGABIDKSDFVFRCNLPPI
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TGISFKYYQTLKESKRQKYLFPPRYTRHALLENFRYKGYTAYRLSTGLMLAPAFSRAN
TGISFKYYQTLKESKRQKYLFFPRYTRHALLENFRYKGYTAYRLSTGLMLASVAVEL

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// Acte="unnamed protein product; putative waskly similar to SIALYLTRANSFERASE 8 (FRACMENT) [Bos taurus] (SPTR|AAL97018, evidence: FASTY, 50.3%1D, 98.7%length, match=489)"
// Codon start=1
// protein id="mac39167.1"
// Ab_xref="G1:26351461"
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/db_xref="taxon:10090"
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/tissue type="lung"
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/dev_stage="13 days embryo"
                                                                                                                                                                                                                                                                                                                                                  Length 3292;
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Pred. No. 0;
0; Mismatches 20; Indels
                            l. .3292
/organism="Mus musculus"
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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Best Local Similarity 99.3%;
Matches 3022; Conservative
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| 11.1 | TATTAACATTGTAATGTTGTTTCAAGTTTACCATCT 3070 AAACGTATTAGCTTCAGAAATTTATCAGAAGTTCATA 2993 AAACGTATTAGCTTCAGAAATTTATCAGAAGTTCATA 2993 AAGCCTTTTTGTTAATAAAAAAAATTATTATTTT 3053 AAGCCTTTTTTGTTAATAAAAATAAATTATTTTTT 3190 TTTGCTGCTGCTAATGAACCTAATTAGCTTTAAATT 3113 TTATGCTGCTGCTAATGACCTAATTAGCTTTAAATT 3120 TTATGCTGCTGCTAATGACCTAATTAGCTTTAAATT 3120 TTTCAATCATGATGAACCTAATTAGCTTTAAATT 3250 TTTCAATCATGCTGTTTAGC 3155 | 820 bp mRNA linear EST 12-JAN-2005 NIH BMAP_IBO Mus musculus cDNA clone equence.) ata; Craniata; Vertebrata; Euteleostomi; hontoglires; Glires; Rodentia; hridae; Murinae; Mus. | alth, Mammalian Gene Collection (MGC) g, Ph.D. gov ames Lin University of Iowa Dr. M. Bento Soares, University of Iowa Dr. M. Bento Soares, University of Iowa Tibution information can be found at Estribution/mouseff.html ed by the Brain Molecular Anatomy Project | usculus" "10090" 945902" Orn (1,5,15 days)" (T1 phage resistant)" e, Vector: pYX-Asc; Site 1: EcoR 1; he library was constructed according the And Soares, Genome Research, 6:791-806, RNA was size fractionated on a 1% agarcee | cDNA synthesis was primed with Oligo-dT ga Not I site. Double strand cDNA was cording to mRNA size fraction, ligated tor, digested with NotI and then cloned to pYX-Asc vector. The library tag between the Not I site and the polyA tail his library was created for the University my Project (BMAP): 'Gene Discovery in the Nervous System', supported by National tal Health (NIMH)." |
|------------|---|--|--|---|---|
| Comparison | | CX565877 N U1-M-LBO-CAM-M-15-0-UI.z IMAGE:30945902 5', MRNA CX565877 CX565877.1 GI:57592906 EST. Mus musculus (house mous Mus musculus (house mous Bukaryota; Metazos; Chor Mammalia; Butheria; Bu | National Institutes of Fi Unpublished (1999) Contact: Robert Strausbe Email: cgapbs-r@mail.nih Tissue Procurement: Dr. cDNA Library preparatic CDNA Library Arrayed by DNA Sequencing by: Dr. Clone Distribution: Dis http://genbme.ulowa.edu/ This clone was contribu | seq primer; para-5. ce 1. 0810 1. 0820 | gel.Firet stran primer containi size selected a size selected a directionally i sequence locate is AATATAGG, iowa Brain Anat Developing Mous Institute of Me |
| | | RESULT 4 CX565817 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISI | TITLE JOURNAL COMMENT | FEATURES SOUR | ORIGIN |
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RESULT 5 BG919404 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

CGAP_Mam6"
nmary; Vector: pCMV-SPORT6; Site_1: Sall;
loned unidirectionally. Primer: Öligo dT.
ted by Life Technologies. Investigator
s: Jeffrey Green, M.D., NIH" 152 343 403 523 223 283 212 272 463 332 cacificeregrificeagaacaacacifecagiges 392 583 452 643 512 703 92 gov by Green M.D. i. Life Technologies, Inc. The I.M.A.G.E. Consortium (LLNL) e Genomics, Inc. clone distribution information can be E. Consortium/LLNL at: ACAGAGAAATGCAAAGATCTGCAATATAGCTTGAAC SCAAGCAGAAGAATATGACAATTTTAGAGCAAAACTG GACTTCGTGGTTTCCCAGACAACACTCCAGTGGGG GICTCTCTGCGGAGCAGAAATTGATAAATCTGACTTC BACAACCCCGGTACCACGCACCAGGAACAGCACATAT STACTCTGAGGATGACTACCTCCAGACCATCACAAAC SCAAGCAGAAGAATATGACAATTTTAGAGCAAAACTG GCAAGAACACATCCCCATTCGAGAGAACATTTTC AGCAAGAACACATCCCCATTCGAGAGAACATTTTC rGTGGACTATCCCTATAACCAGTGTGCAGTGGTT rrrerecacrarcecraraaccagrecagreerr h.gov/. alth, Mammalian Gene Collection (MGC) GAGGGAAGCAGAGACACCAGTGGTACCTCAGCT Gaps ö nontoglires; Glires; Rodentia; Iridae; Murinae; Mus. re 760.4; DB 2; Length 812; d. No. 1.6e-185; Mismatches 11; Indels 0 rgin" Filtrating ductal carcinoma" nthe" column: 23 p: 795. ers aculus" g, Ph.D. 10090" 47286" Sciurognathi, Murcidea, In the Muscidea, I (bases 1 to 812)

National Institutes of Hall Unpublished (1999)
Contact: Robert Strausbeg, Email: Capbbe-remail.nih gortact: Robert Strausbeg, Email: Capbbe-remail.nih gortach Library Preparatio: CDNA CDNA CDNA CDNA CDNA CONTINUE COUNTY (Limage. 11nl. Gov. Blate: LibAM0896 row: n critical Library Requence of Dorganisms—Muschaller (Library Pape—"Rush (Ab) xref="taxon") (Ab) xref="taxon") (Ab) xref="taxon") (Ac) Gov. Buttains—FVBANT (Ab) xref="taxon") (Ac) Gov. Buttains—FVBANT (Ac) Gov. Buttains—FVBA Sc Library constru providing sampl GCTTCCTGTTGCGATGCCATTC GGTAATGGGGGAATTCTCAACA TCTTTATCTAACAAACGAGAC GCACTGAAGACACTCTGGAGCC GCACTGAAGACACTCTGGAGCC rcrrrarcraacaaaccacac ATACAGAGATGCCCATGGAACC 524 ACTAACATGAGCTACGAGGTGG acraacargagcracgaggrag CACATGTTTCCAGTGTCGCAGC cacaretriccaererecaede ccreccecrecaegergrea ccccanachiccccccrcrrch CTGGATGAGAGACAACCCAAA ö ch 24.0%; 1 Similarity 98.6%; 767; Conservative 64 33 93 13 04 64 584 644 24 84 53 44 73 333 393 453 8 8 8 ద ò 812 bp mRNA linear EST 05-JUN-2001 602818295F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4947286 5', BG919404 BG919404.1 GI:14299880 EST. Was musculus (house mouse) Mus musculus Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,

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Page 11

| | | Clone distribution: MGC clone distribution information can be found through the I.M.AB. Consortium/LLML at: |
|--|--|---|
| 61 ACAGGCATCTTTTAAAGTCT 965 CTCTTCTCCATCCAGGTACG 121 CTCTTCTCCATCCAGGTACG 1025 ACTGCATACCGCTTGTCCACAG 181 ACTGCATACCGCTTGTCCACAG 182 AACGTGAAGCTCTACGGATTCT 241 AACGTGAAGCTCTACGGATTCT 241 ACGTGAAGCTCTACGGATTCT 241 ACGTGAAGCTCTACGGATTCT 1145 CACCACTACTATGATAACATGT 301 CACCACTACTAACTATGATAACATGT 301 CACCACTACTAACTAACATGT 301 CACCACTACTAACTAACATGT 301 CACCACTACTAACTAACATGT 301 CACCACTACTAACTAACATGT 301 CACCACTACTAACTAACAACATGT 301 CACCACTACTAACTAACAACATGT 301 CACCACTAACTAACAACATGT 301 CACCACTAACTAACAACAACAACAACAACAACAACAACAA | 0 | Clone distribution: MGC found through the I.M.A. |
| 8 8 8 8 8 8 8 8 | QY 1 DP DP QY 1 | |
| 513 GGTAATGGGGGAATTCTCAACAACAACTCTCTGCGGAGCAGAAATTGATAAATCTGACTTC 572 704 GTCTTCAGGTGTAACCTCCCCCCAATCACAGGGGGCGCTAGTAAAGATGTTGGAAGCAA 763 | FERENCE MASSESSION LICEAR MASS MUST MUSTALE CONTRIBUTE ON G03464558 MASSESSION MASSESSIO | 905 ACAGGCATCTTTTAAAGTCTACCAAACACTCAAAAGAGTCAAAAATGAGGCAAAAGGTT 964 |
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Encyclopedia Project of
Genomic Sciences Center
Division of Experimental
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Please visit our web si
further details.
                                        2214 TAAATCTGATCCCAGTAGAATA
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Mammalia; Eutheria; Buar
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/db_xref="taxon
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                                                                                                                  /mol_type="mmNA"
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
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Pred. No. 1.6e-174;
0; Mismatches 1; Indels
http://image.llnl.gov
Plate: LLAM11667 row: 1 column:
High quality sequence start: 5
High quality sequence stop: 749.
Location/Qualifiers
                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 22.7%;
Best Local Similarity 99.6%;
Matches 740; Conservative
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Fax: 801 585 7177
Email: ddunn@genet
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         /tissue_type="lung"
/dev_stage="13 days_embryo"
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//Dos inch orif ce at constant velocity. The sheared DNA was blunt end-rapaired with T4 DNA polymerase and T4 |
//Dolymucleoride | Unise. Adaptor oligonucleorides were |
//Dolymucleoride | Unise. DNA was prepared from a derivative of pWM2 (gild72114|gb]API29072.1), a copy-number inducible derivitive of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The seared, adaptored mouse DNA was annealed to chemically-complement E. coli XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barkar, M., Beacorn, T., Duval, B., Hamil; C., Islam, H., Longacre, S., Mhmoud, M., Meenen, E., Pedersen, T., Neellly, M., Rose, M., Rose R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffelding with paired end reads from 10kb
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Contact: Robert B. Weiss
University of Utah Genom C
University of Utah
Rm. 300, Biomedical Polymer
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Insert Length: 1000 Sd
Plate: 0032 row: M colum
Scap primer: CACACAGGAAACGG
Class: plasmid ends
High quality sequence strp
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GGAGTGGATGTCACAGCATCTCCAAAAAGCCAATA 1342

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Page 15

| | uv73e09.yl Soares mouse NDMS Mus misculus cDNA clone IMAGE:412840 5. similar to TR:P97713 97713 GD3 SYNTHASE; mRNA sequence. 5. similar to TR:P97713 97713 GD3 SYNTHASE; mRNA sequence. 5. similar to TR:P97713 97713 GD3 SYNTHASE; mRNA sequence. 5. similar to TR:P97713 GD3 SYNTHASE; mRNA sequence. 5. similar to TR:P97713 GD3 SYNTHASE; mRNA sequence. 5. similar to TR:P97713 GD3 SYNTHASE; mRNA sequence. 6. similar to TR:P97713 GD3 SYNTHASE; mRNA sequence. 7. similar to TR:P97713 GD3 SYNTHASE; mRNA sequence. 7. similar to TR:P97713 GD3 SYNTHASE; mrna to TR:P97713 GD3 SYNTHA | es similarity on wrong strand 1G boc 1f crs 1.16 crs 1.17 crs 1.18 crs 1.19 crs 1.10 crs |
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| 361 GAGACGGTACTCTGAGGATGAO 381 GAGACGGTACTCTGAGGATGAO 421 GAACCGGCAAGCAGAAGATTAT 481 CATTCAAGATTCGTGGTTTCC 501 CATTCAAGACTTCGTGGTTTCC 501 CATTCAAGACTTCGTGGTTTCC 601 GCTGGAAAGCAAGAAACATT 601 GCTGGAAAGCAAGAAAACATT 621 GCTGGAAAGCAAGAAAACACATT 621 GCTGGAAAGCAAGAAAACACATT 621 GCTGGAAAGCAAGAAAACACATT 621 GCTGGAAAGCAAGAAAAAAAAAAAAAAAAAAAAAAAAAA | uv73e09.yl Soares mouse N similar to TR:P97713 9 BE633149.1 GI:9915837 EST. Mus musculus (house mouse) Musmalia, Butharia, Buarh Sciurognathi, Muroidea; ul (bases 1 to 631) NCI-CGAP http://www.ncbinning.ndp.ndp.ndp.ndp.ndp.ndp.ndp.ndp.ndp.ndp | Possible reversed clone: Seq primer: -40RP from G High quality sequence at Location/Qualif 1. 631 . 631 |
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| 7 | cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/. Location/Qualifiers 1. 625 / organism="Mus musculus" / mol_type="mRNA" / strain="C57BL/6" / db xref="taxon:10090" / clone="9530036E06" / dex="mala" / tissue_type="urinary bladder" / dev_steage="adult" / clone lib="RIKEN full-length enriched mouse cDNA library, C57BL/6J urinary bladder male adult" | 19.1%; Score 604; DB 7; Length 625; |
| ACCESSION VERSION VERYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL PUBMED COMMENT | FEATURES SOURCE ORIGIN | Query Matches 60 Matches 60 Qy 1 Db 21 Qy 121 Db 141 Qy 181 Qy 241 Qy 241 Qy 241 Qy 241 Qy 301 Qy 331 Db 321 |

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Direct Submission

Computational Analysis Full-Length Mouse cDNAs Compared with Human Genome Sequences Mam. Genome. 12, 673-677 (2001)

Normalization and subfurction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (1), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pippeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods or the mouse full-length cDNA encyclopedia: real-time equence Clustering for construction of a nonredundant cDNA librar. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepar and sequenced in Mouse Genome Exploration Research Group in Riken Genomic Sciences Center and Sequenced in Mouse Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided b Dr. John Todd (Dept. of Medical Genetics Wellcome Trust/MRC building Adden rookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web sie (http://genome.gsc.riken.go.jp) for further details.
enhard, B., Lyons, P.A., Maglott, D.R.,
I.I., McKenzie, L., Miki, H., Nagashima, T.,
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C., Semple, C.A., Setou, M., Shimada, K.,
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H. Ka, A., Hashizume, W., Imotani, K., Ishii, Y.,
Yanaki, Y., Sakai, K., Sasaki, D., Shibata, K.,
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Ano, M., Ohsato, N., Salto, R., Sakazume, N.,
K., Shibata, K., Shiroki, T., Tagami, M.,
ca iki, A., Muramatsu, M. and Hayashizaki, Y.
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Laboratoryr for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yochhama Institute
The Institute of Physica and Chemical Research (RIKEN)
The Institute of Physica and Chemical Research (AIKEN)
The Institute of Physica and Chemical Research (AIKEN)
Tel: 81-45-503-922
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Analysis of the mouse train
of 60,770 full-length CDPAR
Nature 420, 563-573 (200)
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Sciurognathi, Muroidea; Muridae; Murinae; Mus.
1 (Dases 1 to 663)
S (Mazaki,Y., Puruno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikado,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
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Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng
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CDNA Library Arrayed by: The I.M.A.G.E.
CDNA Library Arrayed by: The I.M.A.G.E.
Clone distribution: MGC clone distribution information can letter, //image.llnl.gov
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115 GGGGTCGGTTAAATTCTGATCCAGTAGAATAACTTCAGGGTACCTATTTCAAGGAAAGAA 774
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/clone="IMAGE:503963"
/lab_host="DH10B (TI phage-resistant)"
/clone=lib="NOI CGAP Kid14"
/note="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |
                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Buarchontoglires, Glires, Rodentia, Sciurognathi, Murcidea, Muridae, Murinae, Mus.

1 (bases 1 to 771)
1 (bases 1 to 771)
1 National Intelfunction, inth gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrad by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM11110 row: d column: 12
High quality sequence stop: 645.
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                                                            TTAATTICACAATTAAAACTAGTAAATGAACCA 2297
                                                                                 TTACAGTCCCATTAACAAATAGTAAATGACCCA 807
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                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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/strain="FVB/N"
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May 31, 2006, 10:17:18 ; Search time 1881 Seconds (without alignments) 11735.321 Million cell updates/sec
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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| | Description | Adc73012 Murine ST | Adc73014 Human ST8 | Aah77592 Human sia | Adv69200 Human cel | Abv78252 Human GD3 | Abz35828 Human GD3 | Abx10071 Human GD3 | Ab191793 Human pol | Aag77831 Human alp | Adr24998 Breast ca | Aat03694 Human alp | Adb58122 Toxicity- | Aah34115 Human col | Aba56318 Human foe | Aba45804 Human bre | Aak29997 Human bon | Abs04570 Human gen | Aba68901 Human foe |
|-----------|--------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | ΩI | ADC73012 | ADC73014 | AAH77592 | ADV69200 | ABV78252 | ABZ35828 | ABX10071 | ABL91793 | AAQ77831 | ADR24998 | AAT03694 | ADB58122 | AAH34115 | ABA56318 | ABA45804 | AAK29997 | ABS04570 | ABA68901 |
| | | 10 | 10 | 4 | 13 | 9 | 9 | 9 | 9 | 7 | 13 | 7 | 10 | 4 | 4 | 4 | 4, | 9 | 4 |
| | Query Match Length DB | 3166 | 1500 | 2008 | 840 | 101 | 101 | 1011 | 101 | 2117 | 2117 | 1704 | 1223 | 1511 | 448 | 448 | 448 | 448 | 428 |
| de | Query Match | 100.0 | 29.4 | 23.5 | 19.4 | 7.1 | 7.1 | 7.1 | 7.1 | 7.1 | 7.1 | 7.0 | 6.5 | 5.5 | 4.2 | 4.2 | 4.2 | 4.2 | 4.1 |
| | Score | 3166 | 930.2 | 744.8 | 614.8 | 224.4 | 224.4 | 224.4 | 224.4 | 224.4 | 224.4 | 222.2 | 207 | 175.4 | 131.4 | 131.4 | 131.4 | 131.4 | 130.8 |
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| agtaccagaatttgaaggagaagaaagcacagttttt | 941 GGAGGACATCTCCACCTATGGAGATCCCTCCTCCTGCCAGGATTTTCCTATCGGGC 900 11 | 961 GGTTCTTCTTCCATCCCAGGT | 1021 GGTGATCCCATTGTCCATTGTCATTGATTGATTGCAAGTGTCGCTGTGGAACTGTGT 108 1021 GGTGACTGCATACCGCTTGTCCATAGGCTTGATGATTGCAAGTGTCGCTGGGAACTGTG 108 | 1081 TGAAAACGTGAAGCTCTACGGATTCTGGCCTTTCTCTAAGACTATCGAAGACCTCCACT 114 1081 TGAAAACGTGAAGCTCTACGGATTCTGGCCTTTCTCTAAGACTATCGAAGACACCCCACT 114 | 1141 CAGTCACCACTACTATGATAACA GITACCTAAGCATGGTTTCCACCACATGCTAAGA 1141 CAGTCACCACTATGATAACATACCTAAGCATGGTTTCCACCACGATGCCTAAAGA | 1201 ATACAGCCAATGCTCCAGCTCCATATGACAGGATCCTCAAACTGCAATTG | 1261 TGAAACGCTTAACGTTTCTTAGAAGGAATAATTTCAGAAGGGGAGGGA | Oy 1321 CAGCATCTCCAAAAGCCAATAAAAGGCAAGAAAAGCATGAATTACAAAGGCT 1380 | OY 1381 CTCCCACTTGTCTAGACCAAAGGTACCCGCCCCACTCACT | OY 1441 CTCATTCTCACCTTCATTCTTCTGAGAATAGAGACCAAAACATCAGACTTGGAT 1500 | NATCATCATAGAATITGATTGAGCCAGGGTCTCTCA 156 | TGATAGCCATTCCCACCTTTATCAGAGTGGTAATGAA | Qy 1621 ACTGTGCAATTGTGCCAAAGACGTTTTCTGAAGAATGTCTGAATCATGCGCGGGTTT 1680 | OY 1681 TTACACACAGCTCTTCCTTTATAATAATCCTTCCCATTCTCCCTCC | QY 1741 GAAACAAAATACCTTGATGATTAGGAAGAAAAGTCTTTTTACTTAGCAATGTGCCTG 1800 | Qy 1801 CITCIGATICAGIICGCTIGIGIA AITAAGCIGGGIITGGGIICGGATITGGGC 1860 1801 CITCIGATICAGIICGCTIGIGA AITAAGCIGGGIITGGGIITIGGIICGAIIIGGGC 1860 | 0.00 L |
|---|---|--|--|--|---|---|---|---|--|---|---|---|--|--|--|---|--|
| K Claim 2; SEQ ID NO 2; 97pp; Japanese. | vention relates to a coside alpha2,6-sialylt ficity and selectivity attic, virucide, autili applicable in drugs i infection, inhibiting irrent sequence is that | X 2 Sequence 3166 BP; 937 A; 706 C; 645 G; 878 T; 0 U; 0 Other; | Query Match Best Local Similarity 100.0%; Score 3166; DB 10; Length 3166; Best Local Similarity 100.0%; Pred. No. 0; Matches 3166; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | Oy 1 CGGAGCGGCGAGTGCCGCCCGGGCTTCGCCCCGGCAGCTTTGGCGGCAGG 60 | Qy 61 ACGCCCGTGGCTCAGGATGAGATCGGGGGGCACGCTGTTCGCCCTCATAGGCAGCCTGAT 120 Db 61 ACGCCCGTGGCTCAGGATGAGATCGGGGGGCACGCTGTTCGCCCTCATAGGCAGCCTGAT 120 | Qy 121 GCTGCTGCTCCTGCTATGCTCTGGTGCCCAGCCGACGGCCTGCTCCAGGCT 180 Db 121 GCTGCTGCTCTGCGTATGCTCTGGTGCCCAGCCGACGCGCTGCCCGCTCCAGGCT 180 | Qy 181 GTTGATGGAGGAAGCAGAGACACCAGTGGTACCTCAGCTGACGACTGAAGACACTCTG 240 Db 181 GTTGATGGAAGGAAGCACAAGAGAACACCACTAGCTCAGCTGCACTGAAGACACTCTG 240 | Qy 241 GAGCCCGACAACCCCGGTACCACCACCACCACACACACAC | 301 CCAAATAACAGAAAAGACAAAGATCTGCAATATAGCTTGAACTCTTATCTAACAAAC 101 [| 361 GAGACGGTACTCTGAGGATGACTCCCAGACCATCACAAACATACAGAGATGCCCATG 4 361 GAGACGGTACTCTGAGGATGACTACCAGACCATCACAAACATACAGAGATGCCCATG 4 361 GAGACGGTACTCTGAGGATGACTACCTCCAGACCATCACAAAACATACCAAGAAAAACAACAACAAAAAACAAAAAAAA | 421 GAACCGCAAGCACAAATATTTAGAGCAAAACTGCTTCCTGTTGCGATGC 421 GAACCGCAAAGCAGAAAATTTTAGAGCAAAACTGCGTTCCTGTTGCGATGC 421 GAACCGCAAAAGCAAAAAATATTAGAAAAAAGCAAAAACTGCGATGC | 481 CATTCAAGACTTCCTAGAACACACACACACAGTGGGGACTAACATGAGCTACGA 481 CATTCAAGACTTCCTGTTTCCCCAGAACAACACTCCAGTGGGGACTAACATGAGCTAACGA | 541 GGTGGAAAGCAAGAAACATCCCCATTCGAGAGAACATTTTCCACATGTTTCCAGTGTC | 541 | | Db 661 CAACAAGTCTCTGGGGAGCAGAAATTGATAAATCTGACTTTGAGGTGTAACTT 720 Oy 721 CCCCCAATCACAGGGGGGGGTTAAAAGATGTTGGAAGAAAAAAAA | Db 721 CCCCCAATCACAGGGAGCGCTAGTAAGATGTTGGAAGCAAACAAA |

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| AGECCCAATACTAGATTCTGCCCTTCTAAAACTGTAGAAGACTACCTGTC 1156 AAAAATGTGAAGCTGTTAGGATTCTGCCCTTCTCTAAAACTGTAGAAGACTACCTGTC 1156 AGTCACCACTACTATGAACATTCTGCTTCTCTAAAACTGTTCCACCAGATGCCTAAGAAA 1216 AGCCAATCACTATTATGACACACACACACACACTTCCACACTTCCACACATCT 1261 TACAGCCAGATCCTCCAACTTCCATAGAAGGAATCCTCAAACTGCAATTTAGCCAATTTAGCAATTTTAGCAATTTAGCAATTTAGCAATTTAGCAATTTAGCAATTTTAGCAATTTTAGCAATTTTAGCAATTTTAGCAATTTTAGCAATTTTAGCAATTTTAGCAATTTTAGCAATTTTAGGATG 1336 GTCACAGCATCCCCAAAAAGGAAAAGAAAATTTTAATATAATATAATACAATGGTGA 1336 GTCACAGCATCACAAAAAAAAGGAAAAATTTTAATATAATATAATACAAAGGTGA 1336 GTCACAGCATCCTCCAAAAAAAGGAAAATTTTAAATATAATATAAAAAGGATGA 1336 GTCACAGCATTGTTAAAAAGGAAAAATTTTAAAAAGAATACAAAAGGTAAAAGATACAAAAGATACAAAAAGATACAAAAAAAA | ncer, cytostatic; immunological disease; y; infection; inflammatory disease; ss. | CO LTD. to new kind of polypeptide and hypeptide. 29pp; Chinese. polypeptide, human sialic transferase polypeptide, human sialic transferase polypeptide and a DNA recombination as malignant tumours, nosohaemia, HIV and inflammatory diseases. The ddy directed against the polypeptide. The yeptide of the invention \$51 G; 634 T; 0 U; 0 Other; |
|--|---|--|
| | SULT 3 477592 AAH77592 standa AAH77592; 22-OCT-2001 (f Human sialic tr Human; sialic tr human immunodef Homo sapiens. CN1298005-A.: 06-JUN-2001. 29-NOV-1999; | PR 29-NOV-1999; SPCN-00124142. XX MAO Y, Xie Y, Qiu M; XX MAO Y, Xie Y, Qiu M; XX WPI; 2001-489682/54. DR WPI; 2001-489682/54. P-PSDB; AAG66954. XX Human sialic transferase 27 as one pr polynucleotides encoding this pcm. XX PS Claim 6; Page 21-22 (disclosure); XX CC The invention relates to a nove cc The invention relates to a nove cc Treating various diseases, such as concess to produce the polypeptide cc treating various diseases, such as infection, immunological diseases invention also provides an antipoc cc invention also provides an antipoc XX XX Sequence 2008 BP; 631 A; 392 C; 385 |
| 2 GGAGCGCCGAGTCGGTGCCCCCGGCCTTCGCCCCGGCAGCTTTGGCGGCGGGG 61 17 GGAGCCGCGGGCCCCGGCCCGGCCCCCCCCCCGCGCGCG | 422 AACCGCCAAGCAGAAGAATATTAGAGCAAACTGGCTTCCTGTTGCGATGCC 481 437 AAACGGCAAGCAGAAGAATTTTAGAGCCAAACTTGCTTCCTGTTGCTTGC | 13.7 |

| TITTICAMICATORAGA TITAGITAGE CONTACTGACTCATACAMITITICAL 167 THATTACAMICATORAGA TITAGITAGE CONTACTGACTCATACAMITITICAL 1533 THATCAMANITATICACATACATACATACAGAGCACTCAMAGANITATICATTCTTCTTCTTCTTCTTTCTTTCTTTCTTTTCTTTTTCTTTT | y) protein 27 encoding DNA SEQ ID NO 1. protein 27; cancer; cytostatic; HIV infection; r; gene ds. /qualifiers |
|--|--|
| Db 1008 TCTCATTTTTCCTATAAAC Oy 1514 TAATTTTTCAAATCATAAAC Oy 1574 TTCTATCCATCATCATCATCATCA Oy 1634 GCCAAACACCTTCTTAAACAC Oy 1634 GCCAAACACCTTCTTAAACACAC Oy 1636 CAACATCTCTTCTAAACACAC Oy 1636 CAACATCTCTTCTAAACACAC Oy 1736GAGATCTCTTCTAAACAAAC Oy 1736GCAATGTCCTTCTAAACAAAAC Oy 1736GCAATGTCCTTCTTAAACAAAAC Oy 1736GCAATGTCCTTCTTTTTTCA Oy 1749GCAATGTCCTTCTTTTTTTCA Oy 1740GCAATGTCCTTCTTTTTTTTCA Oy 1741 GTTGAATTTAACTTCTCTCTTTTTT Oy 1967 GTTTCCAGCTTCTTCTCATTTTTTT Oy 1967 GTTTCCAGCTTCTTCTCATTTTTTT Oy 1967 GTTTCCAGCTTCTTCTCATTTTTTTTTTTTTTTTTTTTT | 59200 standard, DNA; 59200; 7EB-2005 (first entr in cell division regulating I division regulating I-HIV; immune disorde sapiens. Location 91834 |
| Deet Match 21.51; Score 744.8; DB 4; Length 2008; Best Local Similarity Si.51; Pred. No. 1.46-184; Best Local Si.51; Pred. No. 1.46-184; Best Local Si.51; Pred. No. 1.46-184; Best Local Si.51; B | |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to inhibiting expression of a target gene (I) in a cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (as1) of dsRNA1 is complementary to (I) and at least port of one strand has an overhang of 1-4 nucleotices. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytokine genes etc. in humans, also genes in Plasmodium or in viruses or viroids that are pathogenic for humans, animals of plants. Introducing an overhang into dsRNA greatly increases effectiveness for inhibiting gene expression, both in vivo and in vitro and also increases stability and thus the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ression inhibitor; oncogene; cytostatic;
                                                                                                                                                                                                                                        TTCTGGAGAACTAAAGGTGTGACTGCATACCGCTTG
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le-stranded RNA complementary to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human GD3 synthase DNA SEQ ID NO
                                                                                                                                                                                                             GGATICIGGCCTTICICTAAGAG
                                                                                                            TCCACAGGCTTGATGATTGCAAG
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     AGGTACCTGAGACACCTCGCTC
                                                   AAGTACCTGAAAGATCTGGCCC
                                                                                                                                               TCCACCGGCTTGATGATCACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA inhibition; dsRNA1; gene (virucide; protozoacide; gene;
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26-OCT-2001; 2001DE-01055280.
29-NOV-2001; 2001DE-01058411.
07-DEC-2001; 2001DE-01060151.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human cell division regulating protein 27, the polynucleotide encoding it, preparing the polypeptide by DNA recombinant techniques, application of the polypeptide in treating diseases, such as cancer, human immunodeficiency virus (HIV) infection, immunopathy and the antagonist of the polypeptide and its medical action and application of the polynucleotide. The present sequence is that of the human cell division regulating protein 27 encoding DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide-human cell disintegrate regulatory protein 27 for treating cancer, human immunodeficiency virus infection, and immunopathy.
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                             "cell division regulating protein
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Pred. No. 1.3e-150;
0; Mismatches 137;
                                                                                                                                                                                                                                                                                         (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
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                                                                                                                                             GACAATTCAACTTACTCTCTCTCCCACAGGCACCCCAT---TCCAGCTGCCATTGAAG
                                                                                                                                                                         CAGTGTGCAGTGGTTGGTAATGGGGGAATTCTCAACAAGTCTCTCTGCGGAGCAGAATT
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                                                                    TTCAGGAAACAAATGGAAGACTGCTGCGGACCCTGCCCATCTCTTTGCTATGACTAAAATG
                                                                                        AACACTCCAGTGGGGACTAACATGAGCTACGAGAGAAAGCAAGAAACACATCCCCATT
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                                                                                                                                CGAGAGAACATTTTCCACATGTTTCCAGTGTCGCAGCCTTTTGTGGAGTATCCCTATAAC
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                                                TTTAGAGCAAAACTGGCTTCCTGTTGCGATGCCATTCAAGACTTCGTGGTTTCCCAGAAC
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                             Gaps
                            3,
        Length 1071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAGGAATCCTCAAACTGCAATTCAGCAAATGTGAAACGGCTTAAC 1274
                            0; Mismatches 366; Indels
        Score 224.4; DB 6;
Pred. No. 6.4e-48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA; 1071
        7.1%;
   Query Match
Best Local Similarity 55.3°
Matches 457; Conservative
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The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligoribonoclectides (dernal and II), both with a double-stranded (ds) structure of at most 49 sequential nuclectide pairs. At least part of one strind (S1, S2) of the ds structures in each of dsrNM1 and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded CC RNA inhibition (RNM1). The method is particularly used to treat tumours or infections, especially by Plemodium or viruses/viroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known method using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the cend, stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with interferon. The present sequence is that of a target DNA of the invention
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protozoacide; gene expression; Mhtisense; tumour; infection; Plasmodium; virus; viroid; anti-GPP; human; MIV; human immunodeficiency virus; Hepatitis C virus; human papill ma virus; gene; ds.
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                                 prion genes, or genes expressed in
ly plasmodia) or in viruses or viroids
r plants). Treating the cells with
extent to which dsRNA can inhibit
and the effect is even greater when dsRNA
tability. ABX09936-ABX10075 represent
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The invention relates to a method for inhibiting expression of a target gene (ABL91658-ABL91797) in a cell by introducing at least one oligoribonuclectide that has a double-stranded structure consisting of at most 49 sequential nuclectide pairs, with at least part of one strand cranded segment of 1-4 nt. The method provides oligoribonuclectides for antisense inhibition of gene expression useful e.g. for treating tumours but the oligoribonuclectides may also be directed against genes present in pathogens (e.g. plasmodium or viruses/viroids) pathogenic on humans, animals or plants) or against cytokine, Id, developmental or prion genes the method provides more effective inhibition of gene expression than use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATAAATCTGACTTCGTCTTCAGGTGTAACCTCCCCCAATCACAGGGAGGCGCTAGTAAA 748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting gene expression in cells, useful for e.g. treating tumors, by introducing double-stranded complementary oligoRNA having unpaired terminal bases.
                                                                                                                                                                                                                                                                                    HCV, gene expression, oligoribonucleotide, tumour, pathogen, virus, viroid, cytokine, prion, antisense oligonucleotide, virucide, protozoacide, antibacterial, ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five gene for which markers are listed in the specification, in a cell sample maken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invertion. This sequence corresponds to a marker used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Classifying a breast cancer patient according to prognosis determining the similarity between the level of expression five genes in a cell sample taken from patient, to control
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; prognosis; game expression; diagnosis.
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     CCTAAGCATGGTTTCCACCAGAT
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                                                                                                                                                                                                                                                                                             standard; DNA; 2117
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                                                                                                                                                                                     sialyltransferase. The gene encodes a protein of 356 a.a. The gene (called WP1) was isolated from the human melanoma cell line WM266-4 and cloned into the E.coli plasmid pUC119 to create pUC119.WP1. The gene was instred into the expression vector pAMORGISSc to produce the plasmid pAMORDESAWP1. The missing N-terminal 19 a.a. were inserted into this vector by PCR amplification using the primers AAQ77835-6. Alpha-2,8-sialyltransferase is useful in the production of physiologically active sugar chains e.g. in the conversion of ganglioside GM3 to GD3. (Updated on 25-WAR-2003 to correct PN field.)
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Pred. No. 9.2e-48;
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                                                                                                                                                         Claim 3; Page 63-66; 102pp; Japanese.
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/note= "the sequence of bases 721-766 is missing from the
pecification. Generic codons coding for the amino acid
sequence VDNMKIY- NHSYIYMP have been inserted by the
indexer"
          891 AAATGCGCGGTGGTGGGAAAATGGTGGGATTCTGAAGAAGAGTGGCTGTGGCCGTCAAATA
                                     GATAAATCTGACTTCGTCTTCAGGTGTAACCTCCCCCCAATCACAGGGGGGCGCTAGTAAA
                                                      GATGAAGCAAATTTTGTCATGCGATGCAATCTCCCTCCTTTGTCAAGTGAATACACTAAG
                                                                                        1011 GATGTTGGATCCAAAAGTCAGTTAGTGACAGCTAATCCCAGCATAATTCGGCAAAGGTTT
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CAGTGTGCAGTGGTTAGTAATGGGGGAATTCTCAACAAGTCTCTCTGCGGAGCAGAAATT
                                                                       GATGTTGGAAGCAAAACAAATCTTGTGACTGTCAATCCCAGCATTATAACCCCTGAAGTAC
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                                                                                                              CAGAATTTGAAGGAGAAGAAGCACAGTTTTTGGAGGACATCTCCACCTATGGAGATGCA
                                                                                                                                                  TTCCTCCTCCTGCCAGCATTTTCCTATCGGGCCAACACAGGCATCTCTTTAAAGTCTAC
                                                                                                                                                                                       CAAACACTCAAAAGAGTCAAAAATGAGGCAAAAAGGTTCTTCTTCCATCCCAGGTACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human melanoma; SK-Mel-28; ganglioside 3-synthase; tumour antigen;
detection; Northern blotting; glycosylation; ds.
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                                                                                                                                                                                                                                                                                         A cDNA clone coding for alpha 2 9-sialyltransferase was isolated from a human melanoma SK-Mel-28 cDNA 1 brary and sequenced. The insert codes for a protein having ganglioside 3-synthase activity which is useful as a biochemical reagent. The cDNA is useful for detecting tumour antigen by Northern blot analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1704 BP; 452 A; 377 C; #34 G; 426 T; 0 U; 15 Other;
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tumour antigen by Northern blot
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                                                                                                                       WPI; 1996-072336/08.
P-PSDB; AAR88326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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us-10-501-930-2.rng

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The present invention relates to a method for predicting a toxic effect of a compound. The method comprises preparing a gene expression profile of a tissue or call sample exposed to the compound, and comparing the gene expression profile to a database compound, and comparing the differential expression of the gene indicates at least one toxic effect. The method is useful for predicting at least one toxic effect of compound, predicting hepatotoxicity or the progression of a toxic effect of a compound identifying an agent that modulates the onset or progression of a toxic response, predicting the callular pathways that a compound modulates in a cell, and identifying an agent that modulates at least one activity of a protein. The method and compositions of the present invention using a database of genes having liver toxin-induced liver tissues or cells for drug screening and toxicity markers in liver tissues or cells for drug screening and toxicity markers in the sequence date for this patent did not form part of the princed.
                                                   CCTAAGCATGGTTTCCACCAGATGCCTAAAGAATACAGCCAAATGCTCCAGCTCCATATG 1228
ccerrrrcigacriccanaccaraccadasaarrrcrccaacreragrarcrrcanaa 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to the compound.
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                                                                                                                                                                                                                                                                                                                                                                  Toxic, toxin; gene expression profile; hepatotoxicity; liver;
                                                                                                                                     AGAGGAATCCTCAAACTGCAATTCAGCAAATGTGAAACGGCTTAAC 1274
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                                                                                                                                                                                                                                                                                                                                                                                 screening; toxicity assay; ds.
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2002US-0364045P.
2002US-0364055P.
2002US-0436643P.
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15-MAR-2002; 3
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specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 1223 BP; 281 A; 322 C; 331 G; 289 T; 0 U; 0 Other;

Length 1223;

Score 207; DB 10; Pred. No. 2.6e-43;

6.5%;

Query Match Best Local Similarity

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   ismatches 370; Indels
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675 GGCTTCTGGCCTTCTCTGTGALPTGCATGAGCAGCCCATCAGCCACCACCACTATGAC 734

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TCCACAGGCTTGATGATTGCAA

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GTCGCTGTGGAACTGTGAAAACGTGAAGCTCTAC 1099

557 AACTITCIGCGIAR--ITGGAAAGTICIGGAAAAGIAGAGAWICCAIGCCAAGGGCCTG 614

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Rosen CA;
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                                                    Birse CE,
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                      28-SEP-2000; 2000WO-US026524
                              99US-0157137P
                                  99US-0163280P
                                           (HUMA-) HUMAN GENOME SCI INC
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Matches 372, Conservative
                                                    Barash SC,
                                                            WPI: 2001-235357/24.
                                                                 P-PSDB; AAG74710.
    WO200122920-A2
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Cancer-associated mucleic acid molecules (N) and proteins (P), where the cancer-associated mucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient s genome cexpession by rectifying mutations or deletions in a patient s genome to produce the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.

Sequence 1511 BP; 447 A; 304 C; 332 G; 420 T; 0 U; 8 Other;

sednences nk DR; The invention relates to a single human gene expression in a sample single exon nucleic acid probes mandle exon nucleic acid acid probes mandle exon nucleic a Human genome-derived single exon displaying gene expression in seprees. Spresent sequence is a single exd Note: The sequence data for this specification, but was obtained ftp.wipo.int/pub/published_pd Claim 1; SEQ ID NO 4623; 639pp 0 Human foetal liver single exon (MOLE-) MOLECULAR DYNAMICS INC gene expression in human fetal Sequence 448 BP; 114 A; 112 C; 2000US-00632366. 2000US-0234687P. 2000US-0236359P. 2000GB-00024263. Chen W, 30-JAN-2001, 2001WO-US000669 2000US-0207456P 2000US-00608408 2000US-0180312P 4.2%; llarity 57.4%; Conservative ABA56318 standard; DNA; 448 (first entry) Hanzel DK, WPI; 2001-483447/52. Best Local Similarity Matches 237; Conserv WO200157277-A2. 21-SEP-2000; 2 27-SEP-2000; 2 04-OCT-2000; 2 Homo sapiens 26-MAY-2000; 30-JUN-2000; 03-AUG-2000; 04-FEB-2000; 01-FEB-2002 09-AUG-2001 ABA56318; Query Match sg, AGGIACCIGAGACACCTCGCTCTTTTCTGGAGAACTAAAGGGGTGACTGCATACCGCTTG 1039 3, 619 258 680 GCAGAAATTGATAAATCTGACTTCGTCTTCAGGTGTAACCTCCCCCCAATCACAGGGAGC 739 317 799 377 859 437 919 496 979 556 GCTAGTAAAGATGTTGGAAGCAAAACAAATCTTGTGACTGTCAATCCCAGCATTATAACC TACACTAAGGATGTNGGATCCAAAAGTCAGTTAGTGACAGCTAATCCCAGCATAATTCGG AACCACAGTIACATCTACATGCCTGCCTTTT-CTATGAAGACRGGAACAGAGCCATCTTG 620 CCCTATAACCAGIGIGCAGIGGIGGIAAIGGGGGAATICTCAACAAGICTCTCTGCGGA ccarroaagaaargcgcgcgcgcgcaaargcrgcgarrcrgaagagagrgccrgcgc G-rcadaradargadecadrirreredregargedarcreecreerregades CAAAGGTTTCAGAACCTTCTGTGGTCCAGAAAGACATTTGTGGACAACATGAAAATYTAT GGAGATGCATTCCTCCTCCTGCCAGCATTTTCCTATCGGGCCAACACAGGCATCTCTTTT AAAGICTACCAAACACTCAAAGAGTCAAAAATGAGGCAAAAGGTTCTTCTTTCCATCCC AGGGTTTATTATACACTGTCAGATGTTGGTGCCAATCAAACAGTGCTGTTTGCCAACCCC CTGAAGTACCAGAATTTTGAAGGAGAAAAAGCACAGTTTTTGGAGGACATCTCCACTAT Gaps Score 175.4; DB 4; Length 1511; Pred. No. 5.8e-35; 3; Mismatches 276; Indels 4;

ö be exon nucleic acid probe for measuring derived from human foetal liver. The hay be used for predicting, measuring and amples derived from human fetal liver. The nucleic acid probe of the invention. The prent did not form part of the printed in electronic format directly from WIPO nucleic acid probes useful for analyzing 88 Human; foetal liver; gene expression; single exon nucleic acid probe; CTGCAATTCAGCAATGTGAAACGGCTTAAC 1274 Gaps CITCATAAAATCGGTGCACTGAMATGCAGCTGGACCCATGTGAAGATACCTCAC 849 ; 0 Length 448; Sequence Listing, English. G; 124 T; 0 U; 0 Other; Indels acleic acid probe #4623. Score 131.4; DB 4; Pred: No. 1.18-23; 0; Mismatches 176; CICCATATGAGAGGAATCCICA 1220 RESULT 14 ABA56318 ò

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TTTTTGGAGGACATCTCCACCTATGGAGATGCATTCCTCCTCCTGCCAGCATTTTCCTAT
                                                     29 Trigicia ca de la contra de la contra contra confecta de la contra co
                                                                                                                                                                                                                                                    CAAAAGGTTCTCTTCCTTCCATCCCAGGTACCTGAGACACCTCGCTCTTTTCTGGAGAACT
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30-JUN-2000; 2000US-0060B40B.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-02346B7P.
27-SEP-2000; 2000US-0234559P.
04-OCT-2000; 2000GB-00024263.
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New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                           Rank
                                                           Chen W,
(MOLE-) MOLECULAR DYNAMICS INC
                                                              Hanzel DK,
                                                                                                                      WPI; 2001-496933/54.
                                                           Penn SG,
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the

Claim 1; SEQ ID NO 4499; 327pp + Sequence Listing; English.

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probes with a collection of detentably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The propes are useful for verifying the expression of regions of genomid DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on calls. The microarray of this invention presents a far grater diversity of probes for measuring gene expression, with far less has then expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the print of the printed specification, but was obtained in electronic format directly from WIPO at the print of the print of the printed specification, but was obtained in electronic format directly from with the sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              G; 124 T; 0 U; 0 Other;
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Job time : 1886 secs
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Sequence Sequence Sequence

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Scoring table:

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Searched:

Database

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Sequence 185, App.
Sequence 187, App.
Sequence 181, App.
Sequence 193, App.
Sequence 195, App.
Sequence 199, App.
Sequence 201, App.
Sequence 219, App.
Sequence 2182, App.
Sequence 1829, App.
Sequence 1829, App.
Sequence 1829, App.
Sequence 748151,
Sequence 748151,
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Sequence 748151,
Sequence 1105, App.
Sequence 21173, A
Sequence 6236, Ap
Sequence 1959, Ap
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Sequence 34256, 7
Sequence 2204, Ap
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10-928-446A-193

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10-928-446A-197

10-928-446A-197

10-928-446A-199

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10-928-66A-748151

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10-928-938-1108
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10-363-483A-34256
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100.0%; Pred. No. 0;
tive 0; Mismatches
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| Publication No. US20060057696A1
| GENERAL INFORMATION:
| APPLICANT: TAKASHIMA, Shou
| APPLICANT: TSUJIMOTO, Masafumi
| APPLICANT: TSUJIMOTO, Masafumi
| APPLICANT: TSUJIMOTO, Masafumi
| TITLE OF INVENTION: GLYCOSYLATING FILE REFERENCE: P25687
| CURRENT APPLICATION NUMBER: US/10,501, CURRENT FILING DATE: 2004-07-29
| PRIOR FILING DATE: 2003-01-30
| NUMBER OF SEQ ID NOS: 30
| SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGAGCGGCGAGTCGGTGCCGCGG
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  Best Local Similarity 100.
Matches 3166; Conservative
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ORGANISM: Mouse
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LENGTH: 3166
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1: EMC Celerra SIDS3/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/USIOB_PUBCOMB.seq:*
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                                                                                                                                              May 31, 2006, 15:43:12; Search time 3701 Seconds (without alignments) 10511.390 Million cell updates/sec
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                                                                                                                                                                                                                                                                                      1 cggagcggcgagtcggtgcc.....gctattagcaaaaaaaaa 3166
                      GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-027-632-44555

US-10-027-632-44555

US-10-085-117-66

US-10-172-118-859

US-10-184-339C-136

US-10-184-139C-136

US-10-085-117-65

US-10-085-117-63

US-10-085-117-63
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
Sequence:
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Gaps

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Result ė Š 11111110987654

206.6 175.4 131.4

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| AGANGGCACAGAGAAAGCATGATTACAAAGCGCT 1380 ACCCGCCCCACTCACTTGCACTTACAAAGCGCCT 1380 CACCGCCCCCACTCACTTTGCACTTACAAAGCGCCT 1380 CACCGCCCCCCCACTCACTTGCACTTACAAAGCGCCT 1380 TCTCTGAGAATACACTTTGCACTTGACCTCCACGAGTCA 1400 TCTCTGAGAATACACTTTGACCACCACGAGTCA 1400 TCTCTGAGAATACACTTACACTTGACCACGAGTCT 1500 ATATACATCATACATTTGATTGACCACGCCCACGTT 1680 TTTCTGAAAGAATTTGATTGACCACGCCCACGTT 1680 TTTCTGAAAGAATTTGATTTGACCCACGCCCACTT 1680 TTTCTGAAAAACCTTCCCCTTTATCAAGTGCTACAA 1620 TTTCTGAAAAACCTTCCCCTTTATCAAGTGCTACAAAAA 1620 TTTCTGAAAAAACCTTCTCCCCTTATTACAATGAAGTACA 1680 TTTTCTGAAAAAACCTTTATTACTTAGACAAGGTACTACAA 1620 TTTTTTCTAAAAACCTTCTCCACTTATTAGAAACAAAAAA 1620 TTTTTTTTCTTAAAAGTTTTACTTAGACAAGAATAAA 1680 TTTTTTTTCTTAAAAGTTTTTACTTAGAAAAAAAAA 1680 TTTTTTTTCTTAAAAGTTTTTACTTAGAAAAAAAAA 1680 TTTTTTTTCTTAAAAAAAAAAAAAAAAAAAAAAAAAA |
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| 1321 CAGCATCTCCAAAAAGCCAATAG 1321 CAGCATCTCCAAAAAGCCAATAG 1331 CTCCCACTTGTCTCAACCAAGG 1331 CTCCCACTTGTCTCAACCAAGG 1341 CTCCACTTCTCACCTTCAACGTTCCAAGGC 1350 AAGTAAAATGAATATTTTCCAGCAAAAGCCAAAGGC 1551 GAATGCTTCCACTTGTTCTAACGATCCAAAGGC 1551 GAATGCTTCCACTTGTTCCAAGGCCCAAAGGCC 1551 GAATGCTTCCACTTGTTCTAAGGCCAAAGGCC 1551 GAATGCTTCCAATTGTGCAAAAGGCC 1551 GAATGCTTCCAATTGTGCAAAAGGCC 1551 AAGTAAAATTGTGCAAAAGGCCAAAGGCC 1551 AAGTAAAATTGTGCAAAAGGCCAAAGGCC 1551 AAGTAAAATTGTGCAAATTGTTCTAATAGGCCAAAAGGCCC 1551 AAGTAAAAATTGTGCAAATTGTTCTAATAGGCCAAAAGGCCC 1551 AAGTAAAAATTGTGCAAATTGTTTTTTTTTTTTTTTTTT |
| 11 GTGATGGGGGAAACCCAGAGACACCCAGTGGTACTCAACCCCTGAAAGACACTCTG 21 GAGCCGGAAACCCCGGTACACCCCGCGAAACCCCGTGAAGACACCCTG 21 GAGCCGGAAACCCCGCTACACCCCCCCCCAGACACCCCCCCC |

| US-10-501-930-4 Query Match Query Match Best Local Similarity 78.4%; Pr Matches 1169; Conservative 0; Qy 2 GGAGGGGGGAGTCGGTGCCCC Db 17 GGAGCGCGAGTCGGGCCCCC Ov 62 CGCCGTGGCTCAGGATGAGAT | 122 137 137 197 197 242 242 253 | 317 377 422 482 497 497 557 557 602 | |
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| Oy 2401 TGTGAGGCTACGCTAAAACCTCTGGGTAGGGAGAGAGTACAGTGCATGAGTGTGGCGGGCT 2460 | TTGAGTAAAATTTGAGTAGATGTTAAATATGAACATTTTATACCTCTTA 2 TTGAGTAAAATTTGAGTAGATGTTAAATATGAACATTTTATACCTCTTA 2 TTGAGTAAAATTTGAGTAGATGTAAATATGAACATTTTATACCTCTTA 2 CCGACACCTTTTAATGTAAGCACATTTATTTATTAATGTACTTGACATT 2 CCGACACCTTTTAATGTAAGCACATTTTATTAATAAGTTACTTGACATT 2 CCGACACCTTTTAATGTAAGCACATTTTATTAATAAGTTACTTGACATT 2 CTGTATATTCTGTTCATCCATCGATTTTCCCAAAAAGTAAGAGCATAG 2 CTGTATATTCTGTTCATCCATCGATTTTCTCTTCAAAAGTAAGGCC 2 TACTGCAAGAAAACTATAAATTTACTCTTTAATTCTTACTTGAGCC 2 | | SULT 2 Sequence 4, Application US/10501930 Sequence 4, Application US/10501930 Sequence 4, Application US/10501930 Sequence 4, Application US/10501930 SEQUENCAL INFORMATION: APPLICANT: TAKASHIMA, Shou APPLICANT: TSUJUMYO, Masafumi APPLICANT: TSUJUMYO, Masafumi TITLE OF INVENTION: GLYCOSYLATING ENZYME FILE REFERBENCE: P25687 CURRENT PILING DATE: 2004-07-29 FRICA APPLICATION NUMBER: PCT/JP03/00883 PRICA PAPLICATION NUMBER: PCT/JP03/00883 |

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1. No. 1.5e-229;
fismatches 308; Indels 14; Gaps
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; Sequence 1175963, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
    APPLICAMT: Wangy David G.
    TITLE OF INVENTION: In the Human Genome
    TITLE OF INVENTION: in the Human Genome
    TITLE OF INVENTION: in the Human Genome
    FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10,01,480
CURRENT APPLICATION NUMBER: US 10/215,598
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SEQ ID NO 1175963
; ERNOTH: 810
                                                                          1222 CCATATGAGAGGAATCCTCAAA
                                                                                                570 TCACATGAAAGGAATCCTCAAAQ
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CORGANISM: Homo sapien
US-10-301-480-1175963
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR FILING DATE: 2002-11-21
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTHARE: FASTESQ for Windows Version 4.0
LENGTH: 810
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                                                                                            GAAAACGTGAAGCTCTACGGATTCTGGCCTTTCTCTAAGACTATCGAAGACACCCCACTC
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                  GTGACTGCATACCGCTTGTCCACAGGCTTGATGATTGCAAGTGTCGCTGTGGAACTGTGT
                                       1037 GTGACTGCATACCGCTTGTCCACCGGCTTGATGATCACAGTGTTGCAGTGGAACTGTGT
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65.5%; Pred. No. 1.1e-60;
ative 0; Mismatches 248; Indels 28;
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Publication No. US20060057564A1
GENERAL INFORMATION:
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Best Local Similarity 65.55
Matches 525; Conservative
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Best Local Similarity 67.4%;
Matches 437; Conservative 1
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US-10-027-632-44555
                                                                                                                                                                   LENGTH: 672
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REPERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

PRIOR PELICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-04-20

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 254; DB 7; Length 672;
Pred. No. 1.8e-54;
1; Mismatches 191; Indels · 19;
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FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-39
PRIOR FILING DATE: 1999-02-39
PRIOR FILING DATE: 1999-04-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-38
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Best Local Similarity 67.4%;
Matches 437; Conservative
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US-10-027-632-44555
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                                                                                                                                                     ONS AND METHODS FOR CANCER
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Pred. No. 1.2e-46;
0; Mismatches 366; Indels
                Sequence 66, Application US/10085117
Publication No. US20030232334A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND MISTILE REPERRENCE: 529452000121
CURRENT FILING DATE: 2002-02-27
CURRENT FILING DATE: 2002-02-27
PRIOR PILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66
LENGTH: 1071
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Best Local Similarity 55.3%;
Matches 457; Conservative
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US-10-085-117-66
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| Oy 869 TICCTCCTCGCGAGCATTTTCTATCGGGCCAACACGGCATCTCTTTAAAGTCTAC 928 | Db 769 CGTAGCATTGGAAAGTAGGAATCCATGCCAAGGCCTGTCCACAGGA 828 Qy | RESULT 9 US-10-172-118-859 US-10-172-118-859 i Sequence 859, Application US/1017218 i Publication No. US20030224374A1 GENERAL INFORMATION: APPLICANT: Dai, Hongyue APPLICANT: Linsley, Peter APPLICANT: Roberts, Chris APPLICANT: Roberts, Chris APPLICANT: Van de Vijver, Marc APPLICANT: Daimonseis and Prognosis of Breast Cancer Patients ITILE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients FILE REFERENCE: 9301-175-999 CURRENT FILING DATE: 2002-06-14 PRIOR APPLICATION NUMBER: US/10/72,118 PRIOR PILING DATE: 2002-06-14 PRIOR PILING DATE: 2002-06-14 NUMBER OF SEQ ID NOS: 2699 SEQ ID NOS: 2699 LENGTH: 2117 | ORGANISM: Homo saptems |
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| OY 1169 CCTAAGCATGGTTTCCACCAGATGCCTAAAGATACAGCCAAATGCTCCAGCTCCATATG 1228 Db 949 CCCTTTTCTGGCTTCCATGCCATGCCGAGGAATTCTCCAACTCTGGTATCTTCATAAA 1008 OY 1229 AGAGGAATCCTCAAACTGCAAATGTGAAACGGCTTAAC 1274 Db 1009 ATCGGTGCACTGAGATGTGAAAGGGCTTAAC 1274 Db 1009 ATCGGTGCACTGAGATGTGAAAGATACTCAC 1054 | RESULT 8 US-10-384-339C-136 Sequence 136, Application US/10384339C Publication No. US20040175703A1 GENERAL INFORMATION: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GE FILE REFERENCE: 20200/2002 CURRENT FILING DATE: 2002-01-03 PRIOR PELLING DATE: 2002-01-03 PRIOR PELLING DATE: 2001-01-09 PRIOR APPLICATION NUMBER: DE 10100586.5 PRIOR APPLICATION NUMBER: DE 10155280.7 PRIOR APPLICATION NUMBER: DE 10155280.7 PRIOR PILING DATE: 2001-10-26 PRIOR PILING DATE: 2001-10-26 PRIOR PILING DATE: 2001-10-26 PRIOR PILING DATE: 2001-10-26 PRIOR PILING DATE: 2001-11-20 PRIOR PILING DATE: 2001-11-20 | | |

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114 ITCAGGAAACAAATGGAAGACTQ#TGCGACCCTGCCCATCTCTTTGCTATGACTAAAATG
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                                        CAGAATTTGAAGGAGAAAAGCACAGTTTTTGGAGGACATCTCCACCTATGGAGATGCA 868
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GENERAL INFORMATION:

APPLICANT: Morris, David W.

APPLICANT: Engelhard, Eric K.

TILLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER; FILE REFERENCE: 529452000121

CURRENT FILING DATE: 2002-02-27

PRIOR APPLICATION NUMBER: US 09/798,586

PRIOR PILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 361

SOFTWARE FEATSEQ FOR Windows Version 4.0

SEQ ID NO 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.1%; Score 224.4; DB 7; Length 2117; 55.3%; Pred. No. 1.8e-46; ive 0; Mismatches 366; Indels 3;
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Matches 457; Conservative
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NISHI, TATSUNAKI
TITLE OF INVENTION: '-2,8-SI
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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; Sequence 1, Application US/10430325

; Publication No. US20040002138A1

; GENERAL INFORMATION:

APPLICANT: SASAKI, KATSUTOSE
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STREET: 1100 NORTH GI
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
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Pred. No. 1.8e-46;
0; Mismatches 366;
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APPLICANT: Roberts, Christopher U,
APPLICANT: Roberts, Christopher U,
APPLICANT: Van (* Veer, Laura Johann
APPLICANT: Van (* Veer, Laura Johann
TITLE OF INVENTION: Diagnosis and Pro-
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: US/10/34/
CURRENT FILING DATE: 2003-01-15
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
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CAAACACTCAAAGAGTCAAAAA
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Best Local Similarity 55.3%;
Matches 457; Conservative (
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APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
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US-10-342-887-859
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US-10-342-887-859
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         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/430,325
FILING DATE: 07-May-2003
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION AUMBER: US/08/361,304A
FILING DATE: 29-NOV-1994
APPLICATION NUMBER: PCT/JP94/00495
FILING DATE: 28-MAR-1994
APPLICATION NUMBER: JP HEI-5-69988
FILING DATE: 28-MAR-1994
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55.3%; Pred. No. 1.8e-46;
tive 0; Mismatches 366;
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NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
STRAIN: WM266-4 cell
CELL TYPE: melanoma
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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TELEPHONE: (703) 816-4000
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TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
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STRANDEDNESS: double
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Matches 457; Conservative
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Publication No. US2003023334A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
TITLE OF INVENTION: NOVEL COMPOSITION:
FILE REFERENCE: 529452000121
CURRENT FILING DATE: 2002-02-27
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 09/798;
PRIOR PILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSEQ for Windows Versi
SEQ ID NO 62
                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGAATTTGAAGGAGAAGAAGG
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                                                                                                                                                                                                                   364 AAATGTGCGGTGGTGGGAAACGC
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; ORGANISM: Mus musculus
US-10-085-117-62
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APPLICANT: Engelhard, Eric K.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER FILE REFERENCE: 529452000121
CURRENT APPLICATION NUMBER: US/10/085,117
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FBELSEQ for Windows Version 4.0
SEQ ID NO 63
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Pred. No. 6.1e-43;
0; Mismatches 375; Indels
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Publication No. US20030232334A1
GENERAL INFORMATION:
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Best Local Similarity 54.2%;
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US-10-085-117-63
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Publication No. US20050287570A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Worth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REPERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
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    Length 1388;
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4; Mismatches 373; Indels
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PRIOR APPLICATION NUMBER: US 6(
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 2140
LENGTH: 1223
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; ORGANISM: Rattus norvegicus
US-11-136-527-2140
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Sequence 322, App
Sequence 949, App
Sequence 1577, Ap
Sequence 166160,
Sequence 166179,
Sequence 596, App
Sequence 498, App
Sequence 498, App
Sequence 3182, A
Sequence 24, Appl
Sequence 22022, A
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81129, A
32, Appl
22022, A
2202, A
226, App
1808, A
15, Appl
75, Appl
1939, Appl
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US-10-488-619-949
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US-10-953-349-3868
US-11-217-529-166179
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US-11-217-529-82562
US-11-293-697-69
US-10-488-619-2492
US-11-242-317-38
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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No.
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| Sequence 589, App Sequence 477, App Sequence 477, App Sequence 4458, Ap Sequence 7683, Ap Sequence 7683, Ap Sequence 62, App Sequence 62, App Sequence 1010, Sequence 1115, App Sequence 115, App Sequence 14579, A Sequence 76, App Sequence 76, App Sequence 76, App Sequence 76, App Sequence 700, App Sequence 700, App Sequence 700, App Sequence 10176, App Sequence 10178, App | ад. | e 42.8; DB 6; Length 1556; No. 0.069; ismatches 72; Indels 0; Gaps 0; TGTGCAGTGGTAGTGATGGGGAATTCTCAACAG 667 | 9 livan, P.C. rial DNA Polymorphisms, Haplogroups, Associations Conditions, And Genotyping Arrays 88,619 |
|---|--|---|--|
| 1-293-697-589 70-196-749-477 70-529-126-99 70-217-529-4458 70-217-529-1030 70-217-529-1030 70-217-529-106168 70-217-529-106176 70-217-529-106176 70-203-697-1714 70-203-697-1714 70-203-697-1714 70-203-697-1714 70-203-697-1714 70-203-697-1714 70-203-697-1714 70-203-697-1700 70-203-697-700 70-203-697-700 70-203-697-700 | LIGNMENTS 28 COET Research et THELIAL GENES 505,928 3,019 | | |
| - SU - SU - SU - SU - SU - SU - SU - SU | 10505: 41 50r Cc 1 END 10/10/ 1-27 60/36 | Scc Pre O; Naacck ATTGR ATTGR ATCGR | 04886 nd Su ochor gical s/10/ |
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| | 28-322 322, Applicatic 322, Applicatic 00 No. US200600 NPORMATION: T: Ludwig Inset: INVENTION: LAW RERENCE: 2807/JM APPLICATION NUM PLILING DATE: 2002 F SEQ ID NOS: 8 F SEQ ID NOS: 8 1556 H Homo sapiens | | 19-949/c 949, Application US/104886 NO NO. US20060099578A1 NFORMATION: T: Greenlee, Winner and Su INVENTION: Human Mitochon INVENTION: Physiological ERENCE: 98-01 WO APPLICATION NUMBER: US/10/ FILING DATE: 2004-03-01 |
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| 00000000000000000000000000000000000000 | SULT 1 -10-505-92 Sequence 3 Sequ | i-10-505 Query M Best Lo Matches | ULT 2 10-486 equenc ublica ENERAL APPLIC TITLE TITLE FILE F |
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Pref. No. 0.59;
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PUBLICATION NO. US2006009612A1
GENERAL INFORMATION:
APPLICANT: SUNYORY LIMITED
APPLICANT: NAKAWIAN, NORTHISA
APPLICANT: NAKAWIAN, NORTHISA
APPLICANT: FUJIMURA, TOWOKO
TITLE OF INVENTION: METHODS FOR ANALY
FILE REFERENCE: S-38-28
CURRENT APPLICATION NUMBER: US/11/217
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US/11/217
CURRENT FILING DATE: 2005-09-02
PRIOR PRIDE OF SEQ ID NOS: 197023
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 166160
  FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10,991
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 3868
LENGTH: 781
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                                                                                                                                                   TYPE: DNA
CRGANISM: Arabidopsis thaliana
US-10-953-349-3868
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Conservative
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Best Local Similarity
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TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
FILE REPERENCE: 98-01 WO
CURRENT APPLICATION NUMBER: US/10/488,619
CURRENT FILING DATE: 2004-03-01
NUMBER OF SEQ ID NOS: 3040
SOFTWARE: Petentin version 3.1
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Publication No. US20060107345A1
GENERAL INFORMATION:
SELUCANT: ALEXANDROV, Nickolai et al.
ATITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
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1.3%; Score 39.8; DB 6; Length 641;
Best Local Similarity 52.0%; Pred. No. 0.26;
Matches 89; Conservative 0; Mismatches 82; Indels (
                                                                                                                                                                         Length 541;
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0.24;
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Pred. No. 0.
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Publication No. US20060099578A1
GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 3040
SOFTWARE: Patentin version 3.1
SEQ ID NO 949
LENGTH: 541
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                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-949
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LENGTH: 641
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 166179, Application US/11217529
Eublication No. US20060099612A1
GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHHIRO
APPLICANT: NAKAO, YOSHHIRO
APPLICANT: KODAMA, YUKKO
APPLICANT: KODAMA, YUKKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKANT, TOSHIHIKO
ITILE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: S-38-285
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Pred. No. 3;
0; Mismatches 123;
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CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
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US-11-217-529-166179
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SEQ ID NO 166179
LENGTH: 8391
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Best Local Similarity
Matches 112; Conserv
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Sequence 596, Application US/10505928
Publication No. US20060088532A1
GENERAL INPOMATION:
APPLICANT: Ludwig Institute for Cancer Research et al.

US-10-505-928-596

RESULT 7

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  THELIAL GENES
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Pred. No. 10;
0; Mismatches
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Publication No. US20060105376A1
GENERAL INFORMATION:
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT FILING DATE: 2005-12-05
PRIOR PLING DATE: 2005-12-05
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: 9498
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Pred. No. 1.9;
0; Mismatches
                FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10,505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/313,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SEQ ID NO 596
LENGTH: 70665
                                            505,928
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; Publication No. US20060107345A1
; GENERAL INFORMATION:
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TITLE OF INVENTION: LYMPHATIC END
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1.2%;
Best Local Similarity 52.1%;
Matches 85; Conservative
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Best Local Similarity 52.5*;
Matches 83; Conservative
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CRGANISM: Homo sapiens
US-10-505-928-596
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APPLICANT: VAN ANDEL INSTITUTE
APPLICANT: VAN ANDEL INSTITUTE
TILLE OF INVENTION: Carcinoma: Propnosis and Drug Target Identification
FILE REFERENCE: 38345-170094
CURRENT APPLICATION NUMBER: US/0/473,173
CURRENT FILING DATE: 2003-09-29
PRIOR PILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 498
SOFTWARE: Patentin version 3.2
LENGTH: 37426
                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/10473173
Publication No. US20060088823A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Microarray General Expression Profiling in Clear Cell Renal Cell
TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification
TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification
CURRENT APPLICATION NUMBER: US/10/473,173
CURRENT FILING DATE: 2001-09-29
PRIOR APPLICATION NUMBER: US 60/279,411
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 498
SOFTWARE: Patentin version 3.2
SEQ ID NO 24
LENGTH: 2296
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   374 AAGTTTCTTTCGTTATCATATAGTCTTCTGGGATTTCTTCTATGGAATTCATGATCTCC 315
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Pred. No. 4.9;
0; Mismatches 83; Indels
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47.9%; Pred. No. 24;
tive 0; dismatches 113;
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50.98; Pre
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                                                                                                              3078 TATGCTGCTGCTAATGAACCTA/
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Sequence 3.5 Application US/1047317
Publication No. US2066008823A1
GENERAL INFORMATION:
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Best Local Similarity 50.9
Matches 86; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT PAPLICATION WIMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 35182
LENGTH: 1837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 CGCCCGTGGCTCAGGATGAGATCGGGGGGCGCGCTGTTCGCCCTCATAGGCAGCCTGATG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 GCCAGCGCGCTCGGGCGGTGCGATCGCTGCGCGGCGGAGCCTGCGAGGCAGCCGGTGG 275
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Publication No. US20060099612A1

GENERAL INFORMATION:
APPLICANT: SUNTORY LIMITED

APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: PUJIMURA, TOMOKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REPERENCE: S-38-285
CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR PULING DATE: 2006-09-02
PRIOR PULING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PAREATIN VERSION 3.3
SOFTWARE: PAREATIN VERSION 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GGAGCGGCGAGTCGGTGCCGGCCCGGGCTTCGCCCCCGGCAGCTTTGGCCGGCGAGGA
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OTHER INFORMATION: a, c, g, t, unknown, or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.2%; Score 36.6; Di
Best Local Similarity 53.1%; Pred. No. 3.4;
Matches 78; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Zea mays subsp. mays US-10-953-349-35182
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us-10-501-930-2.rnpbn

| Db 18605 GGCACAGATGAATTAACATTTATAGATTTTTTTTTTTTATGGAGTGAATAT 18546 Qy 2948 TAGCAAATCAACGTATTAGCAAATTTATCAGAAGTTCATATATAAAATTGC 3007 Db 18545 AAGGATATGCCAAATTTTAAAAATGAATCACATATTCTTACTATTTTTCTTT 18486 Qy 3008 AAAGGGTAAAAGGCTTTTTTGTTAAATAAAAAATAAATTATTTTTTTT | Matches 77; Conservative 0; Mism Qy 2881 ATACAGTGTCACCTTGTATTTALCATT Db 3791 ATTGGGTTTCATTTGGATTGGATG Qy 2940 TTGTTTATAGCAAATGAAAGTATTA Db 3851 TTGTTTTATAACAAATGAAAAGTATTT Qy 3000 TATTTGG 3007 | Mismatches 50; Indels 1; Gaps 1; LATITGIAATGITGITTTCAAGITTACATCT-CTITCA 2939 |
|--|--|--|
| 22022 22. Application US/10953349 DRWATION: ALEXANDROV, Nickolai et al. ALEXANDROV, Ni | SULT 15 -10-488-619-1510 Sequence 1510, Application US/10488 Sequence 1510, Application US/10488 Shication No. US200600957841 SEREAL INFORMATION: APPLICANT: Greenlee, Winner and Su TITLE OF INVENTION: Human Mitochon TITLE OF INVENTION: Physiological CURRENT APPLICATION UNMBER: US/10, CURRENT FILING DATE: 2004-03-01 SEQ ID NO: 3040 LENGTH: 510 LENGTH: 510 LENGTH: 510 LENGTH: 510 LENGTH: 510 LENGTH: 510 LENGTH: 510 LENGTH: 510 LENGTH: 510 LENGTH: 510 LENGTH: 510 | 11van, P.C. Arial DNA Polymorphisms, Haplogroups, Associations Conditions, And Genotyping Arrays 488,619 |
| Query Match 1.1\$; Score 36; DB 6; Length 1241; Best Local Similarity 51.9\$; Pred. No. 3.9; 3.9; Indels 0; Gaps 0; Matches 81; Conservative 0; Mismatches 75; Indels 0; Gaps 0; QY 2898 ATTAACATTGTATCATGTTTCAAGTTAACATCTTTTTTTT | Query Match Best Local Similarity 52.3%; Pred. Natches 79; Conservative 0; Aismotches 79; Abachara Activity Carlabar Concord 0; Aismotches 79; Abachara Activity Carlabar Concord 0; Aismotches 79; | # 35.8; DB 6; Length 510; 1. No. 2.6; 4. No. 2.6; 4. No. 2.6; 4. Indels 0; Gaps 0; 4. CAAGITTACATCITICATTCITIATAGCAAATC 2956 4. Indels 1 |
| US-10-505-928-226 US-10-505-928-226 Sequence 226, Application US/10505928 Publication No. US20060088532A1 GENERAL INFORMATION: TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES FILE REFERENCE: 30867/39178 CURRENT APPLICATION NUMBER: US/10/505,928 CURRENT FILING DATE: 2004-08-27 PRIOR PAPLICATION NUMBER: US 60/363,019 PRIOR FILING DATE: 2002-03-07 NUMBER OF SEQ ID NOS: 866 SOFTWARE: Patentin 3.2 SEQ ID NO 226 LENGTH: 4908 TYPE: DNA GOGANISM: Homo sapiens 1.11%; Score 36; DB 6; Length 4908; GOURTY MATCH GOUETY MATCH GOUETY MATCH GOUETY MATCH RESULT 4908 1.11%; Pred. No. 8.5; RESULTION OF SEQUENCE TO SET TO SECOLOR OF TO SECONOR OF TO SECONOR OF TO SECONOR OF TO SECONOR OF TO SECONOR OF TO SECONOR OF TO SECONOR OF TO SECONOR OF TO SECONOR OF TO SECONOR OF TO SECONOR OF TO SECONOR OF TO SECONOR OF TO SECONOR OF T | Search completed: May 31, 2006, 19:18 56 Job time : 51 secs | |

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Sequence 2130, Ap
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Sequence 13872, Ap
Sequence 12178, A
Sequence 26413, A
Sequence 26414, A
Sequence 26414, A
Sequence 26415, A
Sequence 26415, A
Sequence 26415, A
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1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
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8: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/PCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/BCOMB.seq:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-949-016-26414
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US-08-95-742-4
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| US-68-989-545-8 US-68-989-16-16412 US-68-98-016-16412 US-68-68-708B-22 US-10-170-097-651 US-11-170-097-651 US-22-2463-14 US-68-22-463-14 US-68-22-463-14 US-68-22-463-14 US-68-22-463-14 US-68-22-463-14 US-68-25-48-23 US-68-25-48-33 US-68-949-016-1610 US-68-949-016-113921 US-68-949-016-113921 US-68-949-018-13259 US-68-949-002-786 US-68-949-002-786 US-68-949-018-1280 US-68-949-016-1280 US-68-949-016-13894 US-68-949-018-13894 US- | ## IGNMENTS /09949316 HISMS IN KNOWN GENES ASSOCIATED WAN DISEASE, METHODS OF DETECTION AND USES THEREOF ### 14 78 8 /231, 48 8 \$ Vereion 4.0 | *; Score 224.4; DB 3; Length 1756; *; Pred. No. 2.9e-50; 0; dismatches 36; Indels 3; Gaps 1; CTTCCTCTTGGGATGCCATTCAAGACTTCGTGGTTTCCCAGAAC 508 AAGACTGTGGGACCCTGCCATTCTTTGTATGCTAAATGG 423 CTAACATTAAGCTACGAGGGGAAAGCAAAAACAATTGCTAT 483 | CCAGTGTCGCAGCTTTTGTGGACTATCCCTATAC 62 CCAGTGTCGCAGCCTTTTGTGGACTATCCCTATAC 62 |
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| 24 51.2 1.6 1682 3 25 51 1.6 95890 3 26 228 50.2 1.6 20674 3 29 49.8 1.6 20674 3 29 49.2 1.6 20674 3 20 31 49.2 1.6 5000 3 2 32 47.8 1.5 21129 3 34 47.8 1.5 24922 3 2 35 46.6 1.5 24922 3 2 37 45.4 1.4 18651 3 2 45.2 1.4 640681 3 2 45.2 1.4 640681 3 2 45.2 1.4 640681 3 2 45.2 1.4 18759 3 2 45.2 1.4 18759 3 2 45.2 1.4 18759 3 2 45.2 1.4 18759 3 2 45.2 1.4 18759 3 2 45.2 1.4 18759 3 2 45.3 1.4 18759 3 2 45.4 18 115 11569 3 3 45.2 1.4 18759 3 3 45.2 1.4 18759 3 3 45.2 1.4 18759 3 3 45.3 1.4 18759 3 45.4 18 11.4 18759 3 45.4 18 11.4 18759 3 | RESULT 1 US-09-949-016-2130 Sequence 2130, Application US/099450 Patent No. 6812339 GRERAL INFORMATION: APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: WITH HUMAN DIR FILE REFERENCE: CLO01307 CURRENT APPLICATION NUMBER: US/09/900RRNT FILING DATE: 2000-04-14 PRIOR APPLICATION NUMBER: 60/241, 78 PRIOR PILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR PLING DATE: 2000-10-03 PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012 SOFTHARE: FRAKESEQ for WINGOWS VETELS LENGTH: 1756 TENGRANISM: HUMAN US-09-949-016-2130 | Query Match Best Local Similarity 55.3 Matches 457; Conservative 449 TTTAGAGCAAACTGG 10 | |

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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 29-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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APPLICANT: ASARI, KATSUTOSHI
APPLICANT: MUNRA, KAZUMI
APPLICANT: HANAI, NOBUO
APPLICANT: HANAI, NOBUO
APPLICANT: NISHI, TATSUNARI
TITLE OF INVENTION: '-2,8-SIALYLTRANSFERASE
NUMBER OF SEQUENCES: 7
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FILING DATE: 28-MAR-1994
APPLICATION NUMBER: JP HEI-5-69988
FILING DATE: 29-MAR-1993
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Mismatches 366; Indels
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REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-66
TELECOMUNICATION INPORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEFAX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARATERISTICS:
LENGTH: 2117
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Best Local Similarity 55.3%;
Matches 457; Conservative
                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
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1049 TTGATGATTGCAAGTGTCGCTG
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ORGANISM: Human
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                                                                                               Sequence 436, Application US/09949016
Fatent No. 6812339
GENERAL INPORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION WINBER: G0/241,755
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: G0/241,755
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
FRIOR FILING DATE: 2000-09-08
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FRIOR FILING DATE: 2000-09-08
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7.1%; Score 224.4; DB 3; Length; 55.3%; Pred. No. 3.2e-50; tive 0; Mismatches 366; Indels
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Best Local Similarity 55.3?
Matches 457; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Human
                                                                                       US-09-949-016-436
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Sequence 13872, Application US/0994016

Fatent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/0241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FBSEESEQ for Windows Vergion 4.0
SEQ ID NO 13872
LENGER 137394
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134413 CACAGTTACATCTACATGCCTGCGTTTTTCTATGAAGACAGAACAGAGCCATCTTTGAGG 134472
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1311 cirrirciograficacacircipscroicionala asersacarciarides as o
                                                                                                                                                                         CCTAAAGAATACAGCCAAATGCTCCAGCTCCATATG 1228
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                                                        CCTTTCTCTAAGACTATCGAAGACACCCCACTCAGTCACCACTACTATGATAACATGTTA
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Pred. No. 4.4e-26;
0; Mismatches 208;
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LOCATION: (1)...(137394)
OTHER INFORMATION: n = A,T,C or
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Best Local Similarity 55.9%;
Matches 264; Conservative
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US-09-949-016-26413/c
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                                                                                                                                                                                                                       Sequence 12179, Application US/09949016

| Sequence 12179, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| CURRENT APPLICATION NUMBER: 60/241,755
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR APPLICATION NUMBER: 60/237,768
| PRIOR APPLICATION NUMBER: 60/231,498
| PRIOR PLLING DATE: 2000-10-03
| PRIOR PLLING DATE: 2000-10-03
| PRIOR PLLING DATE: 2000-10-09-09
                                                   134713 GTCTTACCCTTTTCTGGCTTCCATGCCCATGCCCGAGGAATTTCTCCAACTCTGGTATCTT 134772
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            1163 ATGTTACCTAAGCATGGTTTCCACCAGATGCCTAAAGAATACAGCCAAATGCTCCAGCTC 1222
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                                                                                                                         134773 CATAAAATCGGTGCACTGAGAATGCAGCTGGACCCATGTGAAGATACCTCAC 134824
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                                                                                              CATATGAGAGGAATCCTCAAACTGCAATTCAGCAAATGTGAAACGGCTTAAAC
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0; Mismatches 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.4%; Score 139.2; 55.9%; Pred. No. 4.46
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)...(137743)
OTHER INFORMATION: n = A,T,C or G
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LOCATION: (1)...(13774:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                              RESULT 5
US-09-949-016-12178
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LENGTH: 137743
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 05/0294,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
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APPLICANT: VENTER: J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
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Pref. No. 3.2e-18;
1; Mismatches 155;
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Patent No. 6812339
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Patent No. 6812339
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PRIOR APPLICATION NUMBER: 60/241,
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,
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Best Local Similarity 55.9%;
Matches 198; Conservative
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; ORGANISM: Human
US-09-949-016-72793
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Best Local Simi
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Sequence 26414, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITTLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-010-03

PRIOR PILING DATE: 2000-00-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 26414
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                                                                                                                                                       3.3%; Score 105.6; DB 3; Length 601; ilarity 55.9%; Pred. No. 3.2e-18; Conservative 1; Mismatches 155; ThAble n
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                                                                                                                                                                               ed. No. 3.2e-18;
Mismatches 155;
     NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 72792
LENGTH: 601
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Best Local Similarity 61.1%;
Matches 162; Conservative (
                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .09-949-016-26414/c
                                                                                   ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-72792
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GENERAL INCRMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER: PRIOR FILING DATE: 2000-09-08
NUMBER: PRIOR FILING DATE: 2000-09-08
SOUTWARE: FRASESQ for Windows Vergion 4.0
SEQ ID NO 72793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VENTER, J. Craig et al. IIILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DIREASE, METHODS OF DETECTION AND USES THEREOF
                                                                  CTCCAGCTCCATATGAGGGAATCCTCAAACTGCAA 1249
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481 GAGCAGCCATCAGCCACCACTALTATGACAACGICTTACCCTTTTCTGGCTTCCATGCC 422
                                                                                                                                 421 ATGCCCGAGGAATTTCTCCAACTTTGGTATCTTCATAAAATCGGTGCACTGAGAATGCAG 362
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Pred: No. 9.3e-17;
0; Mismatches 103;
                                                                                                                                                                                                C 1274
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Patent No. 6812339
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; Sequence 26415, Application US/09949016
; Patent No. 681233
; GENERAL INFORMATION:
                                                                     1190 ATGCCTAAAGAATACAGCCAAAT
                                                                                                                                                                                                                                                           361 CTGGACCCATGTGAGGATACCT
                                                                                                                                                                                                1250 TTCAGCAAATGTGAAACGGCTTA
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TGATAACATGTTACCTAAGCATGGTTTCCACCAGAT 1191
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600 AAGTAGAGGAATCCATGCCAAGGHCCTGTCCACAGGACTTTTTCTGGTGAGCGCAGCTCT 541
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dismatches 269; Indels
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FRASE
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Pred: No. 5e-11;
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Sequence No. 5798244

GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gal,
TITLE OF INVENTION: SIA' 2,3Gal,
TITLE OF INVENTION: SIA' 2,3Gal,
TITLE OF INVENTION: SIA' Z,3Gal,
TITLE OF INVENTION: SIA' Z,3Gal,
TITLE OF INVENTION: SIA' Z,3Gal,
TITLE OF INVENTION: SIA'Z,3Gal,
TITLE OF INVENTION: SIA'Z,3Gal,
TITLE OF INVENTION: SIA'Z,3Gal,
TITLE OF INVENTION:
STATE: Virginia
COUNTRY: U.S.A.
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MEDIUM TYPE: 1.44 diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/626/95
FILING DATE: April 3, 1996
CLASSIFCATION: 435
FILING APPLICATION DATA:
APPLICATION NUMBER: JP 77469/495
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARROLD TURK
                                                                                                                                                                      540 écercirciérdaagaderecem
                                                                                                                                                                                                                                            1132 CACCCCACTCAGTCACCACTACT
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REFERENCE/DOCKET UMBER: P1.
TELECOMMUNICATION: TELECOMMUNICATION: (703) 716-1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: not relevant
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Best Local Similarity 50.2%;
Matches 283; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1048 bases
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US-08-626-994A-4
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| Sequence 72794, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| APPLICANT: WINTER, J. Craig et al.
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND FILE OF INVENTION NUMBER: US/09/949,016
| CURRENT APPLICATION NUMBER: 60/241,755
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-20
| PRIOR PLILING DATE: 2000-10-33
| PRIOR PLILING DATE: 2000-10-33
| PRIOR FILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOFTWARE: FABECEQ for Windows Version 4.0
| INVENTED OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF TABLES OF T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.2%; Pred. No. 1.25-10, tive 0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 99.8; DB 3;
Pred. No. 1.2e-16;
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        FILE REPERENCE: CL001307
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Best Local Similarity
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ORGANISM: Human
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AGCAGAAATTGATAAATCTGACTTCGTCTTCAGGTGTAACCTCCCCCCAATCACAGGGAG
                                                                  739 CGCTAGTAAAGATGTTGGAAGCAAAACAAATCTTGTGACTGTCAATCCCAGCATTATAAC
                                                                                                                                                                      538 GAAATATTACAACAATCTTTTAACCATTCAGGACCGTAACAACTTCTTCCTCAGTTTAAA
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TITLE OF INVENTION: Sia' 2,3Gala 1,4GlCNAC
TITLE OF INVENTION: SIALYLTRANSFERASE
CORRESPONDENCE: 4
CORRESPONDENCE ADDRESS:
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STREET: 1941 Roland Clarke Place
CITY: Reston
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,994
FILING DATE: April 3, 1996
APPLICATION NUMBER: UP 77469/1995
FILING DATE: April 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARTOLI TURK
REGISTRATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P14595
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1+ (ASCII)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,742
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Patent No. 6017743
GENERAL INFORMATION:
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TELEFAX: (703) 716-1180
INFORMATION FOR SEG ID NO: 4:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 1.44 di
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973 CCATCCCAGGTA---CCTGAGACTCGCTCTTTTCTGGAGAACTAAAGGGGTGACTGC 1029
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                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                         12;
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                                                                                                                                                                                              Score 79.6; DB 3; Length 1
Pred. No. 5e-11;
0; Mismatches 269; Indels
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APPLICANT: Shuichi TSUJI et al.
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4GicNAC '2,8-
TITLE OF INVENTION: SIALYTRANGERASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSES: Greenblum & Bernstmin, P.L.C.
STREET: 1941 Roland Clarke Place
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"YPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
US-08-957-742-4
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Patent No. 5798244
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: MG-DOS
SOFTWARE: Word Perfect 5.1+
CURRENT APPLICATION DATA:
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Best Local Similarity 50.2%;
Matches 283; Conservative
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STATE: Virginia
COUNTRY: U.S.A.
ZIP: 20191
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OF INVENTION:
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TOPOLOGY:
US-08-957-742-2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        722 GAAATATTACAACAATCTTTAACCATTCAGGACCGTAACAACTTCTTCCTCAGTTTAAA 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  485 criciccarraccaaraacriccegiccicciccacarererececerrargaaraa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              619 TCCCTATAACCAGTGTGCAGTGGTTGGTAATGGGGGAATTCTCAACAAGTCTCTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             782 AAAGCTTGATGGGGCCATACTTGGATCCCTGCATTTTTCTTCCACACTTCTGCAACTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08957742
Patent No. 6017743
GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: Sia' 2,3Gala 1,4GlCNAC ' 2,8-
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.5%; Score 79.6; DB 2;
Best Local Similarity 50.2%; Pred. No. 6.4e-11;
Matches 283; Conservative 0; Mismatches 269;
PILING DATE: April 3, 1996
CLASSFFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1090 GAAGCICTACGGATICTGGCCTTT 1113
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                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P14595
RELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 716-1191
TELEPAX: (703) 716-1190
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1660 bases
                                                                   PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: JP 77469/1995
FILING DATE: APRIL 3, 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARNOLD TURK
                                                                                                                                                                                                                                                                                                                                                                         not relevant
                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: not 1
                                                                                                                                                                                                                                                                                                                                                                                            linear
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973 CCATCCCAGGTA----CCTGAGACHCCTCGCTCTTTTCTGGAGAACTAAAGGGGGTGACTGC 1029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           902 TTGGCCTGGAATATCATGCAACHTGTCAACAGGTACTGGAAAAACAAACAACACTGTCACC 961
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Pref. No. 6.4e-11;
0; Mismatches 269; Indels
                                                E: Greenblum & Bernschin, P.L.C.
1941 Roland Clarke Place
                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/626,994
FILING DATE: April 3, 1996
APPLICATION NUMBER: UP 77469/1995
FILING DATE: April 3, 1995
ATOMORE: April 3, 1995
ATOMORE: April 3, 1995
ATOMORE: April 3, 1995
ATOMORE: April 3, 1995
TEGERATION NUMBER: 33,094
REFERENCE/DOCKET NUMBER: P14545
TELEPHONE: (703) 716-1191
                                                                                                                                                                                                                                                                                                (HSCII)
                                                                                                                                                                                                                                                                                              SOFTWARE: Word Perfect 5.1+ (A CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  559 CATCCCCATTCGAGAGACATTT
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                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
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STRANDEDNESS: not relevant
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1660 h...
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NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenblum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                     STATE: Virginia
COUNTRY: U.S.A.
ZIP: 20191
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OY 1030 ATACGCTTGTCCACAGGCTTGATGATTGCAAGTGTCGCTGTGGAACTGTGTGAAACGT 1089

Db 962 CAAACGACTGAGGTATCCTAATGTATACTCTTGCATCTGCAATATGTGAAGAGAT 1021

Oy 1090 GAAGCTCTACGGATTCTGGCCTTT 1113

Db 1022 CCACTTGTACGGTTTCTGGCCCTT 1045

Search completed: May 31, 2006, 14:25:31 Job time : 572 secs